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1943	cg44001328	334	AGCAGCTCCAG GGCCCTGAGTTC CT[G/gap]CCAGA GGCTGGAGAGC AGGCAGCTG	G	gap			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.|pcls:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1944	cg43958501	129	TCACATAGAAAA GCTAAAGACAAA A[T/C]ACTGGTAC CAAACATAGCCC TTAGG	T	C			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:P46926 PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE- 6-PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0060) - HOMO SAPIENS (HUMAN), 289 aa.	1.6E-156	5
1945	cg43958501	19	TTTTTTTTTTTTT TTTTT[A/T]TTTGA AAATACTGGATT TAATAGAA	A	T			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:P46926 PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE- 6-PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0060) - HOMO SAPIENS (HUMAN), 289 aa.	1.6E-156	5
1946	cg44004587	967	TGTTTATCACAG CCTACTAAAAAC A[C/gap]AGAGTT TCACTCATTTGTT CAAATT	C	gap			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1947	cg44004587	1036	GCAAAGATTAAA TTAAGTTTTATTT [G/gap]CTCGCTC TCATTTTACAATA ATCTC	G	gap			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1948	cg44004587	1262	AAAGTCATTCTA AGTTTGTTAAGC A[G/C]ATAAATTT TTCTGTAATCATT TACC	G	C			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	

1949	cg44004587	282	GTACAATTTTTAACATTAATATACA[C/T]ATTCCATAATCTCATCTATTTAACA	C	T			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1950	cg44004587	378	TTCCTGACTCTGTAGGACAGTGGTC[C/gap]TCAGTTGGGGGTTGACTCTGTCCCC	C	gap			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1951	cg44004587	573	ACCGAGTGGGACTCAATTCCCATTT[T/gap]ATGAACACCTCTGTGCTCACTGTAA	T	gap			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1952	cg44004587	783	ATATCATTTAATTTCCCTTGAACCT[gap/T]GCTCTGCTAGTTTAATCTGCTAATA	gap	T			SILENT-NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1953	cg43255138	882	CGTGTCCATGGCGGGGGTTCTCCAA[T/C]ACACTCACACTGTCCATGTTCTTTT	T	C			SILENT-NONCODING	isomerase	Human Gene Homologous to SWISSPROT-ID:Q00688 RAPAMYCIN-SELECTIVE 25 KD IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) - HOMO SAPIENS (HUMAN), 224 aa.	1.40E-118	19
1954	cg42711479	676	CTTGAGGAAACTTCGGTTGCAGATT[G/gap]AAGCATTTCAGGTTGTGCATTTTGT	G	gap			SILENT-NONCODING	isomerase	Human Gene Similar to SPTREMBL-ID:Q16645 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE - HOMO SAPIENS (HUMAN), 108 aa.	2.90E-54	2
1955	cg42711479	729	GATGCATGTAGTAGCCTTTCCTGAT[G/A]ACAGAACACAGATCTCTTGTTCGCA	G	A			SILENT-NONCODING	isomerase	Human Gene Similar to SPTREMBL-ID:Q16645 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE - HOMO SAPIENS (HUMAN), 108 aa.	2.90E-54	2

1956	cg43919167	986	CCAACCATGTCA AGATGATAAACA A[T/C]TCGCTTAG TACAAGAGATGG ATGCA	T	C		SILENT-NONCODING	isomerase inhibitor	Human Gene Similar to SWISSPROT-ID:P49312 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED) - MUS MUSCULUS (MOUSE), 319 aa.	8.80E-78	5
1957	cg43145505	3397	TTAAACAGCATG CATTGAACTGAA A[A/gap]GATAAC TGAGAAAATGAA AGCTCAC	A	gap		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.|pcls:SWISSPROT-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3
1958	cg43918241	2846	ACCTAGAGAGAG AAAAAATGCTTTT [T/gap]CTTTGTGA AAAATCTGAATT CCTGT	T	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
1959	cg43918241	3412	GCACACAAATGT TGGCAAAGTCAA A[A/gap]CCCCAT GAATTAAAACCT ACTGGAA	A	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
1960	cg43918241	4823	TTCTGTATGTGT GTATATATATATA [gap/T]ATTATGTA CTTCTGGCAATT CTATC	gap	T		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3

1961	cg43983484	2863	GGGACTGTGGTGACTTCTGCTGCTG[G/gap]CCCCGCCCCTGCCCCCAGAGCGTCC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1962	cg43983484	2959	TGTGTGTGAATCTGCTTTTCCTCTG[C/gap]CTTCGGAGGGAAATTGTAAATCCTG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1963	cg43983484	2960	GTGTGTGAATCTGCTTTTCCTCTGC[C/gap]TTCGGAGGGAAATTGTAAATCCTGT	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1964	cg43983484	359	GGCCGGCGGCGGCCCGCCGCGGGGC[G/C]GCGGCGGCGGGGGCACGGTCCCCCG	G	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1965	cg43983484	360	GCCGGCGGCGGCCCGCCGCGGGGCG[G/C]CGGCGGCGGGGGCACGGTCCCCCGC	G	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1966	cg43917863	127	TATACATTCAGATATGTTTGAAACA[C/gap]TTCTTAAGGCTACAAAACAGAACAT	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q08881 TYROSINE-PROTEIN KINASE ITK/TSK (EC 2.7.1.112) (T-CELL-SPECIFIC KINASE) (TYROSINE-PROTEIN KINASE LYK) (KINASE EMT) - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	4
1967	cg43976564	205	CAAACAAATGTACGACAGGTCAGAA[A/G]CTTAAGTTACAAAATAGAGTCAATA	A	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q99683 MITOGEN-ACTIVATED KINASE KINASE KINASE 5 - HOMO SAPIENS (HUMAN), 1374 aa.	0.00E+00	6

1968	cg43976564	307	TAAAAAAACATA AACTTTATACAG T[A/C]ATTGAAAT TACGCATTTCTA CTCAG	A	C			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q99683 MITOGEN-ACTIVATED KINASE KINASE KINASE 5 - HOMO SAPIENS (HUMAN), 1374 aa.	0.00E+00	6
1969	cg43916734	20924	CCTCATTTGGAG GAAAAAAGCAT G[C/T]ATTCTAGC ACAACAAGATGA AATTA	C	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1970	cg43916734	20951	TTCTAGCACAAC AAGATGAAATTA T[G/A]GAATACAA AAGTGGCTCCTT CCCAT	G	A			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1971	cg43916734	20956	GCACAACAAGAT GAAATTATGGAA T[A/G]CAAAAGTG GCTCCTTCCCAT GTGCA	A	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1972	cg43916734	21059	TTAGCTTTTTGTT GTTTTTTTTTTT[g ap/T]CCTTCTAAC ACTTGTATTTGG AGGC	gap	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1973	cg43090990	2252	CCAGAGACAGG AAAGAATTTGCC TT[C/G]TCCCTGG GAACTGGTTCAA GAGACA	C	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10
1974	cg43090990	2718	ATTCCTATCTGT GGATGTGTAAAT G[G/gap]CTGGGG GGCCAGCCCTG GATAGGTT	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10

1975	cg43090990	2726	CTGTGGATGTGT AAATGGCTGGG GG[G/gap]CCAGC CCTGGATAGGTT TTTATGGG	G	gap		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10
1976	cg43956329	2485	GTAACTACAGTG GCATTAGGACTT A[C/T]CGCTTAGA TGACAATAGTGC TCTTT	C	T		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.|pdb:SWISSPROT-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1977	cg43956329	3342	TCTGTAAATGTC AGTGTCTGAACA G[A/gap]CAACAC AAATTCAAATCAT TATACG	A	gap		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1978	cg43956329	3427	ATTAAACCAAAC TCCTGTCCAATT T[C/G]ACTTATAC AACATAGTCAGT CTAGA	C	G		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.|pdb:SWISSPROT-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1979	cg44022982	3348	CAGGGAGGAGG GGAGGTGCAGG GAA[G/A]AGGGG CCGGCCTCAGCT GTCACCAG	G	A		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q16584 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	11

1980	cg44022982	3469	GTCATCTGGGGC CAGGGCTCTCTG G[A/G]TGCCTTCC TGCTGCCCCAGC CAGGG	A	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q16584 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	11
1981	cg42922283	4204	ATGGCTGCCCTC TGGCAGGGCAG GG[T/C]AGGGCA GTGACACTGTAG GAGCATA	T	C			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q99558 NIK, SERINE/THREONINE PROTEIN-KINASE - HOMO SAPIENS (HUMAN), 947 aa.	0.00E+00	17
1982	cg43299934	926	CTTCTCAATAGG ACTACAGTATGG A[G/T]AAAGAAAG GACTTTCTGGAG AGGAC	G	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92667 KINASE A ANCHOR PROTEIN - HOMO SAPIENS (HUMAN), 903 aa.	0.00E+00	17
1983	cg43336163	2707	CGTTGGAAGACT GAGTGCCCGGG GC[A/gap]CAGCA CAGAAGCCGCG CCCACCGCC	A	gap			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1984	cg43336163	2786	GTCTCCGCCCAG CTCCAGTCCTGT G[A/T]TCCGGGC CCGCCCCCTAG CGGCCGG	A	T			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1985	cg43336163	2787	TCTCCGCCCAGC TCCAGTCCTGTG A[T/A]CCGGGCC CGCCCCCTAGC GGCCGGG	T	A			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1986	cg43336163	3208	TCTCGGAGCCCC AGCCGGCTCCG CC[C/G]CCTTCG GCGGTTTGGATA TTTATTG	C	G			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19

1987	cg43336163	3209	CTCGGAGCCCC AGCCGGCTCCG CCC[C/G]CTTCG GCGGTTTGGATA TTTATTGA	C	G			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1988	cg44929725	5014	TCACCAAGGTCT CTGTGTCAAACC T[G/A]TGGCCACT CTATATGCACTT TGTTT	G	A			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
1989	cg42859664	338	AGTGTGGATGCT GGTGGCAGGAG TC[C/A]AGGACTG TGAAGAGCTGTC AGCATA	C	A			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0.00E+00	15 (15q26.1)
1990	cg38810367	4136	AGGTTTCACCAT GATGGCCAGGC TG[A/G]TCTCGAA CTCCTAACCTCA AGTGAT	A	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P52333 TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3) (LEUKOCYTE JANUS KINASE) (L-JAK) - HOMO SAPIENS (HUMAN), 1124 aa.	0.00E+00	19 (19p13.1)
1991	cg43995263	191	AAGATTATAAATA CGAGGGGGTAA G[C/gap]CCCACC TGAGGGCACAG AACCTTTT	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)
1992	cg43995263	194	ATTATAAATACG AGGGGGTAAGC CC[C/gap]ACCTG AGGGCACAGAA CCTTTTCTC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)

1993	cg43995263	2249	ACGTTTCTGAGA ACTGGCTGGGG GC[C/gap]AGGAG GCGGACCACAC GGTGCGGCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)
1994	cg43969763	6070	TTAAGATATCATA TGGGTCAGGTCA [T/gap]TTTTTTTTT TCTGTGCTGGTT GCCAC	T	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1995	cg43969763	6079	ATATGGGTCAGG TCATTTTTTTTTT[gap/T]CTGTGCTG GTTGCCACATCT TAGCA	gap	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1996	cg43969763	6135	CAAAAACTAAA GCAGTTTTTAAA C[C/T]GATATTTA CGTAAAGAAAT CATAA	C	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1997	cg43918966	663	CCTGATAGAGGA AGAGGTGGCAG GG[A/G]AAACTG CCCAGCTCAAAG CCCTAGT	A	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q13308 COLON CARCINOMA KINASE-4 PRECURSOR - HOMO SAPIENS (HUMAN), 1070 aa.	0.00E+00	6 (6p21.1)
1998	cg43019995	3241	GCCCGTGGGAC CATGACTTAGGG AG[G/gap]TGGGA CCCACCCACCCC CATCCAGG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P53667 LIM DOMAIN KINASE 1 (EC 2.7.1.-) (LIMK-1) - HOMO SAPIENS (HUMAN), 647 aa.	0.00E+00	7 (7q11.23)

1999	cg44910735	226	GGGGTGTCTCG GGCAGAGACCC CCG[G/C]GCTTG GGGCAGCTGAG GCGGCCGGG	G	C		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q13869 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE - HOMO SAPIENS (HUMAN), 1149 aa.	0.00E+00	9 (9q34.1)
2000	cg43257904	116	CGGGGGAGACA CAAAAGGGACCC CC[C/gap]AAAAT CCACATGGGGT GCTGGGAAC	C	gap		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2001	cg43257904	141	CAAAATCCACAT GGGGTGCTGGG AA[C/gap]CCCAA AATCCAGTGGAA GGCACATC	C	gap		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2002	cg43257904	2476	CGGACTCTCGTT ATTGGCTCTGCG G[G/gap]ACTCAG CCTTCCACCCTT ATTGGGT	G	gap		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2003	cg43257904	267	AATTTAGAAGTA TCCCCAAAGCCA A[gap/A]GAGGAA ACCAAATGATGG AGGAGAC	gap	A		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2004	cg43257904	318	AGGGGGCTCAG TCTTTGGCGGGG GT[C/gap]CCCCA ATTCCAGAAGAA CTGGAAAA	C	gap		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)

2005	cg43257904	38	TTTTTTTTTTTTT TATTTTTTTTTTT /G]CCCAGCAGAA TTCTGTGCTTCT TGG	T	G		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2006	cg43257904	482	TGAGATTGGCTC CCTGGTGGCTTG G[G/gap]CGGGG CCTAAGGCACAA GGCGGGCT	G	gap		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P10398 A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2007	cg42879455	2335	ATAGTGGCTTCT GAGCAAAGGCC AA[A/G]AAATTAT TGTGCCTGAAAT TTCCCG	A	G		SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0.00E+00	X (Xq21.3)
2008	cg43016269	6151	TACATCATCTGG CCAGGCATGGTC G[gap/C]TTACGC CTGTAATCCTAG CACTTTG	gap	C		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q28021 RHO-ASSOCIATED KINASE - BOS TAURUS (BOVINE), 1388 aa.	0.00E+00	
2009	cg43931272	1166	TTAGGGATAAAA CACTAACTCTAG T[G/C]CCTTTAAC GGGCAATAGCAA CTTTT	G	C		SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2010	cg43931272	1452	CCTCACTCAGAG CAGCCACACACA G[T/G]GGCCGTT GACGCTGGAAC CTCGGGC	T	G		SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	

2011	cg43931272	307	GGCTAATTTTTATA[A/G]ATGGCGTTTCACCATGTGGACCAGA	A	G			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2012	cg43931272	959	TCTCAGTACTCCCACTCAATTTTTT[gap/T]CCTACTGAGATGAGGGAAGCAATT	gap	T			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2013	cg44003408	253	GGACTGGAGACTGATGCATGAGGGG[G/C]CTACGGAGGCGCAGGAGCGGTGGTG	G	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P53355 DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1) - HOMO SAPIENS (HUMAN), 1431 aa.	0.00E+00	
2014	cg44001122	4440	AGTGTTTGGGTTTTGTTTTTTCTTT[A/G]AGAAAAAGAAATGTACACCACTCCT	A	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P31152 EXTRACELLULAR SIGNAL-REGULATED KINASE 4 (EC 2.7.1.-) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK) - HOMO SAPIENS (HUMAN), 557 aa.	4.40E-307	18
2015	cg43957153	131	GGGACCGGCGGCGGCGGCA[G/C]CGGCGGCGGTGTTTTAAC	G	C			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)
2016	cg43957153	132	GGACCGGCGGCGGCGGCGGCAG[C/G]GGCGGCGGTTTAACT	C	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)
2017	cg43957153	81	AAGTGACGATACTTTTGGCGCGCGC[C/gap]GGTTGCTGTTTCTTCTCTGGCTCCG	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)

2018	cg44004766	3864	CAGATTCGAAATTCTGTGCCATGGC[A/G]TATATGTTCAAATTCAAACCATTTT	A	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2019	cg44004766	4255	TGTATAGTAGGGATAAAACACTAAC[T/gap]TAATGTGTATTCATTTTAAATTGTT	T	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2020	cg44004766	4256	GTATAGTAGGGATAAAACACTAACT[T/gap]AATGTGTATTCATTTTAAATTGTTC	T	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2021	cg43952792	322	CGCCGGGCCGGGGACACCCCGGCGC[C/gap]GCCCCCTCGGTGCTCTCGGAAGGCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2022	cg43952792	351	CCCTCGGTGCTCTCGGAAGGCCCAC[C/gap]GGCTCCCGGGCCCGCCGGGACCCCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2023	cg43952792	367	AAGGCCCACCGGCTCCCGGGCCCGC[C/gap]GGGACCCCCCGGAGCCGCCTCGGCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2024	cg43952792	377	GGCTCCCGGGCCCGCCGGGACCCCC[C/gap]GGAGCCGCCTCGGCCGCGCCGGAGG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)

2025	cg43952792	383	CGGGCCCGCCG GGACCCCCCGG AGC[C/gap]GCCT CGGCCGCGCCG GAGGAGGGCG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2026	cg43952792	388	CCGCCGGGACC CCCCGGAGCCG CCT[C/gap]GGCC GCGCCGGAGGA GGGCGGGGAG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2027	cg43952792	559	TATAAAGTTTGT GATCGTTGGCG GA[A/C]ATTTTGG AATTTAGATAAT GGGCTG	A	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2028	cg43971741	2104	TGAGCACAGTTA TGGCAGAGAAGT T[T/gap]CTCCGC ACCAGAATTATC CACAGCA	T	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2029	cg43971741	2108	CACAGTTATGGC AGAGAAGTTTCT C[C/gap]GCACCA GAATTATCCACA GCAACTT	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2030	cg43971741	2133	CGCACCAGAATT ATCCACAGCAAC T[T/gap]GGCTGA GCCCCACTACAC ACAGAGA	T	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2031	cg43971741	2161	CTGAGCCCCACT ACACACAGAGAA A[T/C]CATCAACC TGACTTAAGAGT TTTCA	T	C			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9

2032	cg43971741	2162	TGAGCCCCACTACACACAGAGAAAT[C/T]ATCAACCTGACTTAAGAGTTTTCAA	C	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2033	cg43971741	2196	GACTTAAGAGTTTTCAAGATGTCAA[A/gap]CTTCAGGCTGATCAGCAGATGGGAT	A	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2034	cg43971741	2234	CAGCAGATGGGATGTGAAAAATACT[A/gap]CCCTATTCTATCATTTGCTGTTGCT	A	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2035	cg43971741	2506	ATTATAGTTCATGTCATTGAAAGTT[T/gap]AAATTGGTTTCATTTAAAGATCAAT	T	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2036	cg43971741	2516	ATGTCATTGAAAGTTTAAATTGGTT[T/gap]CATTTAAAGATCAATATACTAGGTC	T	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2037	cg43971741	2521	ATTGAAAGTTTAAATTGGTTTCATT[T/gap]AAAGATCAATATACTAGGTCTGCCT	T	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2038	cg43119489	2360	GGTCTCAGCGGCCGGCAGACGTGAG[G/gap]CGCTTCCGAGCGCAGGCCTCCGCCG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00537 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.70E-282	

2039	cg43119489	2376	AGACGTGAGGC GCTTCCGAGCG CAG[G/gap]CCTC CGCCGCCACAG CCGCCTTCCG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00537 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.70E-282	
2040	cg43123314	2399	TGGACATTCCTA GGAAACCCAGA GG[G/gap]TGGAG GTGGGGGCCCC ACGGCTAAA	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q16875 6-PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105) / FRUCTOSE-2,6-BISPHOSPHATASE (EC 3.1.3.46) BRAIN/PLACENTA-TYPE ISOZYME (6PF-2-K/FRU-2,6-P2ASE) - HOMO SAPIENS (HUMAN), 520 aa,|pdb:SPTREMBL-ID:Q16875 FRUCTOSE 6-PHOSPHATE,2-KINASE/FRUCTOSE 2,6-BISPHOSPHATASE (EC 3.1.3.46) (FRUCTOSE-2,6-BISPHOSPHATASE) (FRUCTOSE-2,6-BISPHOSPHATASE) - HOMO SAPIENS (HUMAN), 520 aa	1.80E-281	
2041	cg43921754	153	CCGCGCCACCC CGGCCCCGCG CCA[gap/G]CAGC CCCTCGCCGCG CGTCCAGCGT	gap	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2042	cg43921754	207	CGGCCAGCAGC CTCCCCATACGC AG[G/gap]TCCTG CTGGACCGCCC CGTCGCGCC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2043	cg43921754	285	AGCTCCGCCGC CCCGAAACTTTC AC[C/gap]GCGAG CGGGAAATATGG GATGTATA	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)

2044	cg43921754	292	CCGCCCCGAAA CTTTCACCGCGA GC[G/gap]GGAAA TATGGGATGTAT AAAATCAA	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2045	cg43922705	178	GAGAGCCTCTCG GCAGGCGGGGG GG[G/gap]TCCTC TCCTCCAGAACA AAAGGCAC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P27987 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
2046	cg44019155	1267	AATCCACGTTTA TTTTTCCTGTGT C[T/C]GAAGTGTT CTATGTAATGAC ATTGA	T	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2047	cg44019155	1317	CTCTCTGAAACT GTCATTTTGAGT C[gap/T]GTTTCA CCTTGCAGGATG CTCACAC	gap	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2048	cg44019155	1317	CTCTCTGAAACT GTCATTTTGAGT C[gap/T]GTTTCA CCTTGCAGGATG CTCACAC	gap	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2049	cg44019155	1363	CACACATCTCCC TCTCCACCTTTTT [T/gap]GCCTTAA ATTCATTAAAAG CATTGC	T	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2050	cg43241753	1017	CCACAGCCCCTT TCTCTGTCTTTTC [C/T]TTTATTTCA GCTACCCATCCA GTGG	C	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9

2051	cg43241753	2525	GCTGCACCGGC CGCTTTCCCCCA CC[C/gap]GTGCC GGGAGGCCTTC CCTGCGCTT	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9
2052	cg43241753	2530	ACCGGCCGCTTT CCCCCACCCGT GC[C/G]GGGAGG CCTTCCCTGCGC TTGCGGC	C	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9
2053	cg43947749	1615	CTTCCATCTGGG AGCCCCAAGAG GG[G/C]CTGGGA AGGGGGGCCAT AGCCCATC	G	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2054	cg43947749	1616	TTCCATCTGGGA GCCCCAAGAGG GG[C/G]TGGGAA GGGGGGCCATA GCCCATCA	C	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2055	cg43947749	2070	AGGTCTACTCCC TCCTCACCCCAC C[C/gap]TGGAGG GCCAGGGGAGT GGAGAGAG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2056	cg43932396	923	CCCAATGCCACA TTGCGCATAGCT G[C/T]AGAAGTCC TTAACATTTCCCT ACGT	C	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)

2057	cg43932396	409	ACAGGGAGTCA GGGAGGGCCTG GGG[C/gap]GACA GCGGAAAGGTTA AGCGTCGAA	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
2058	cg43932396	480	AGAGATCATCTG AGGGGGAGGCT CC[C/gap]GGTGG GACAGTCACCAA GAACTGTG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
2059	cg43957447	2146	ATGTTGTCATTG ATATAAACCTGT T[gap/T]GGTTCA GCAAACAAACTA AAATGAT	gap	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49336 CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1.-) (PROTEIN KINASE K35) - HOMO SAPIENS (HUMAN), 464 aa.	1.80E-260	
2060	cg43930359	1473	GCATGAGGAGAT GGAGGGCGGGA CT[G/gap]GGCCG CCCAGCCCCTTG ACTCCAGC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.|pdb:SWISSPROT-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.	4E-255	
2061	cg43930359	1511	CCTTGACTCCAG CCTCGACCGCCA G[G/gap]CCCCAG GCCAGAGCCAC CCAATGAA	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.|pdb:SWISSPROT-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.	4E-255	
2062	cg43965549	1595	CCATGTTTGCTC TAAATTAAGACA G[gap/G]CATTGA TCTCCTGGAGGC TGGTTCT	gap	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)

2063	cg43965549	1803	CAGGTGACGTGA TTCTAAGGCAGG A[A/gap]TTTGAG AGTTCACAGAAG GATCGTG	A	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
2064	cg43965549	2199	AAACATTTTATAC TGTACATGCTAT[G/gap]CTGAAGA CATTCAAAACGT GATGTT	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
2065	cg43965549	2282	ATTTTTGTACATC CCAAAGGATGAG [A/C]ATGTGACCT TTAAGAAAAAATG AAAA	A	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2066	cg43965549	2283	TTTTTGTACATCC CAAAGGATGAGA [A/C]TGTGACCTT TAAGAAAAATGA AAAC	A	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2067	cg43965549	2286	TGTACATCCCAA AGGATGAGAATG T[gap/T]GACCTTT AAGAAAAATGAA AACTTT	gap	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)

2068	cg43965549	2485	AGTAGTCTTATG TAAAGTATGTTTT [T/gap]ACATTATG CAAATAAAACCC AATAC	T	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2069	cg43926820	475	TCTCAGCATGAA CTCCTGAGTGAA G[C/G]CTCTCCTC AGCGTGACTCAG GAACA	C	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P51956 SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 3) (HSPK 36) - HOMO SAPIENS (HUMAN), 459 aa (fragment).	1.40E-251	13
2070	cg43329922	119	CTGGCACCTCTG GAGAGGGCAGA GC[C/gap]TCCTC AGAAGAGCTGG CCTGAGGAA	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P23677 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE A (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 461 aa.	1.30E-250	15 (15q14)
2071	cg43292279	1658	CCGAGCCTGAAC TGAGCCCCAGC GG[G/gap]CTGGC GGGCCTTTTTCC TGCGTCCC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN-TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2072	cg43292279	1985	CTGTCCTGCCCG TGAGGGTGGGG GG[G/gap]ACCGG GCCCCTCTCTAG GGACCCCT	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN-TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2073	cg43292279	2181	GCCCACCCGCC TTGTGAGATGGA AT[C/T]GTAATAA ACCACGCCATGA GGACAC	C	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN-TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15

2074	cg43292279	2214	ACCACGCCATGAGGACACCGCCGCC[C/gap]GCCTCGGCGCTTCCTCCACCGAAAA	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN-TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2075	cg43928793	1815	TTCTGTGCCGACCACGCCCCAGGAC[C/gap]TCCGGAGCGCCCTGCAGGGCCGGGC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:Q15831 SERINE/THREONINE-PROTEIN KINASE 11 (SERINE/THREONINE-PROTEIN KINASE LKB1) - HOMO SAPIENS (HUMAN), 433 aa.|pcls:SWISSPROT-ID:Q15831 SERINE/THREONINE-PROTEIN KINASE 11 (SERINE/THREONINE-PROTEIN KINASE LKB1) - HOMO SAPIENS (HUMAN), 433 aa.|pcls:SPTREMBL-ID:Q15831 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 433 aa.|pcls:TREMBLNEW-ID:G2754827 SERINE THREONINE KINASE 11 - HOMO SAPIENS (HUMAN), 433 aa.	4.70E-237	
2076	cg43069976	120	GGTCCCTGGAGCTCCGCACTTGGCG[G/gap]CGCAACCTGCGTGAGGCAGCGCGAC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.|pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

2077	cg43069976	1592	AATGCTGTAGT GTTGAATACTTG G[T/C]TCCATGAG CCATGCCTTTCT GTATA	T	C		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.|pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
2078	cg43069976	1593	AATGCTGTAGTG TTGAATACTTGG T[T/C]CCATGAGC CATGCCTTTCTG TATAG	T	C		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.|pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
2079	cg43069976	1813	TCTAAATCTTGG GAGAAAAAATAA T[G/A]TTAGGAAA AAAATATTTATGC AGGA	G	A		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.|pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

2080	cg43957648	211	GAGCAGACACA GTACCTGATCCA AC[A/G]CCACAA GGCAAATCTATG GCCATCA	A	G		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2081	cg43957648	413	CCAGGCGTAGCT CATGAGGGCCA CG[C/gap]CGGCG GCTGGAGCCCCC CGTGAGCAA	C	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2082	cg43957648	414	CAGGCGTAGCTC ATGAGGGCCAC GC[C/gap]GGCGG CTGGAGCCCCC GTGAGCAAT	C	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2083	cg43957648	418	CGTAGCTCATGA GGGCCACGCCG GC[G/T]GCTGGA GCCCCCGTGAG CAATACTG	G	T		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2084	cg43957648	426	ATGAGGGCCAC GCCGGCGGCTG GAG[C/gap]CCCC GTGAGCAATACT GCTGGGCCA	C	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2085	cg43957648	78	AGGTCTTTATTG AAAGTGGCAGG GG[C/gap]CTCTC AATGTTCTATGA AAACTAAC	C	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2086	cg43957648	79	GGTCTTTATTGA AAGTGGCAGGG GC[C/gap]TCTCA ATGTTCTATGAA AACTAACA	C	gap		SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2

2087	cg43257603	3364	AACTCCAGGTCT AAACAGCTGACC C[G/gap]AGTGAT GGGGAATTTATC CGTGACC	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2088	cg43257603	3368	CCAGGTCTAAAC AGCTGACCCGA GT[G/gap]ATGGG GAATTTATCCGT GACCAATT	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2089	cg43257603	3384	GACCCGAGTGAT GGGGAATTTATC C[G/T]TGACCAAT TTATCCTTGACC AATAA	G	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2090	cg43257603	3386	CCCGAGTGATG GGGAATTTATCC GT[G/T]ACCAATT TATCCTTGACCA ATAACC	G	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2091	cg43257603	3426	GACCAATAACCT AATTGTCTATTC C[G/T]GAGTTATA AAAGTCCCCATC CTTAT	G	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2092	cg43257603	3427	ACCAATAACCTA ATTGTCTATTCC G[G/T]AGTTATAA AAGTCCCCATCC TTATT	G	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2093	cg43257603	3478	AGCTCTACTGGA ATTTTCATACAC G[G/gap]TAAATG CAGAAGTTACTA AGTATTA	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)

2094	cg43257603	3627	ATCAAGGTGACTAAGAAAATCAGTT[G/C]TGTAAATAAAAACAAGCAGCATAAA	G	C			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2095	cg43984889	1176	TCTAGAAAGTTCTATTAGTCGTGAT[A/C]TCGTCTTGTTTTGCTTTGTATTTTG	A	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.|pcls:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	X
2096	cg43984889	696	CTGGGACTAAATCATCAGGGCATGG[C/gap]CACCTGATGTCTTCCACTTTCAGGG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.|pcls:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	X
2097	cg43984889	697	TGGGACTAAATCATCAGGGCATGGC[C/gap]ACCTGATGTCTTCCACTTTCAGGGT	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.|pcls:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.8E-221	X

2098	cg42506800	132	CATCGCCGACTC TGCCCAGACTCT T[A/C]GAGCCGG GGCACCCTCAAA CCCCAG	A	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q16654 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) - HOMO SAPIENS (HUMAN), 411 aa.|pcls:SPTREMBL-ID:Q16654 PYRUVATE DEHYDROGENASE KINASE ISOFORM 4 - HOMO SAPIENS (HUMAN), 411 aa.	1.6E-220	7 (7q21.3)
2099	cg43947829	389	TCATTCCAACAG CTTTACCAGGCT T[C/G]GCCAACC CAATAAGTTACA CACTCA	C	G			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
2100	cg38438124	1574	GCCTCGGACAG ACATGAACATTG GA[G/T]GGACAG AGGTGGCTTCG GTGTAGGA	G	T			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE) (PTDINS(4)P-5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.8E-216	10
2101	cg43917871	1157	AATCAGCCTATT ATAATTTTTTTTT[T/gap]ATGACTGA ACTACTATAAAT CCACA	T	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2102	cg43917871	1201	ATCCACAAGCAA CGGTTCAGACAC G[G/T]TGCTTCTG AAGTGTTTCACC CCTCC	G	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)

2103	cg43917871	1234	GAAGTGTTTCAC CCCTCCCCGCCA G[G/gap]CGCAAG CTGCATCAAGGA GAGGGTG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2104	cg43917871	1241	TTCACCCCTCCC CGCCAGGCGCA AG[C/gap]TGCAT CAAGGAGAGGG TGGACTCCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2105	cg43990838	21	TAGATTTTTTTTT TTTTTTT[A/T]TTG TTGACACAAAAT CTTTTTATTC	A	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q03426 MEVALONATE KINASE (EC 2.7.1.36) (MK) - HOMO SAPIENS (HUMAN), 396 aa.	1.4E-203	12 (12q24)
2106	cg43945404	1579	TAGTAATCATTG GATGCATGATGG G[G/gap]CAGGGC CGGTGATGGTG CCTCCCCC	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2107	cg43945404	1586	CATTGGATGCAT GATGGGGCAGG GC[C/gap]GGTGA TGGTGCCTCCCC CTTGCTGG	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2108	cg43945404	1661	CTTTCACCGCTC ATTATGTAGTCT G[G/gap]CTACAG CCCTCAAAAACA GCTTATA	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2109	cg43945404	1670	CTCATTATGTAG TCTGGCTACAGC C[C/gap]TCAAAA ACAGCTTATACT CTTAAGA	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11

2110	cg43933472	1413	GTGACTAAAGCA ACAGTAAGCAGT A[gap/A]GGTGCA CTGAAGTACATA CTGCCGC	gap	A			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2111	cg43933472	1565	TCCAAACGGCTC AAAGGAGTCAAA G[T/C]GGATAAG CCAAGACGGGC TGGAGAC	T	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2112	cg43933472	634	GATGCTGACATG CTGTAGAAGGAA A[A/C]AGAATTGT ATACTTTCTCATT TAAA	A	C			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL-REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2113	cg42923882	233	CACACATGGGG CTCCCCAGGCAA GG[C/gap]CACCT GCTGACAGAGGT GAAGGCGA	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa.	1.8E-196	
2114	cg43929069	149	AATGAACCAAAT TACCCAAACAAA A[T/G]AAACATGG CAATATAAAAAT GTTAA	T	G			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa. [pcls:SWISSPROT-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa.	1.6E-192	
2115	cg44131795	251	CCACAGGAATTA ACGGAAGAAGTG T[A/G]TACAATTT TTGAGCTATGCT CTTTA	A	G			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G2760825 PROTEIN KINASE C-BINDING PROTEIN BETA 15 - RATTUS NORVEGICUS (RAT), 498 aa.	1.1E-191	

2116	cg43917159	2170	CCATAAGCAGAA CAAGAACCAAAT C[A/gap]AACGTC TTAACGCGTATA GAGAGAT	A	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.2E-191	16 (16p13.3)
2117	cg43917159	2172	TAAGCAGAACAA GAACCAAATCAA A[gap/A]CGTCTT AACGCGTATAGA GAGATCA	gap	A			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.2E-191	16 (16p13.3)
2118	cg43917159	2397	TGCAGAATGTTG TTGGTTACTGTT G[C/gap]TCCCCG AGCCCCTCAACT CGTCCCG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2119	cg43917159	304	AAGCAATTCTAC CTGCCTTGGCCT C[C/T]CAAAGTGC TAGAATTACAGG CATAA	C	T			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2120	cg43917159	320	CTTGGCCTCCCA AAGTGCTAGAAT T[A/G]CAGGCATA AGCCACCACGC CTGGCC	A	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2121	cg42703622	1554	GGAAACTTAGTG TGCCTTGGAAAA G[G/gap]CCGCAA GTTGCTTACTCC GAGTAGC	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
2122	cg44932781	121	AGACCAAATGCA GAGAAGCCGGT AG[G/gap]AACCC GAGGCCACGGA GGCTGCTGG	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:P78356 PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II BETA (EC 2.7.1.68) (1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE) (DIPHOSPHOINOSITIDE KINASE) (PTDINS(4)P-5-KINASE) - HOMO SAPIENS (HUMAN), 416 aa.	2.50E-185	17

2123	cg4393442	936	GCACTGGCAGC CTGCTGTGCAGG GG[C/A]AGCAGC ATCCACAGGGG GCATCCAG	C	A			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G1778153 MAP KINASE 3B - HOMO SAPIENS (HUMAN), 347 aa.	3.20E-183	
2124	cg43987006	123	CCATGATTCAGG GGCACAGCTGC CC[C/gap]AGCAG ACACACACTTTC ATACGCAC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P21425 RIBOSOMAL PROTEIN S6 KINASE I (EC 2.7.1.-) (S6K) (P70-S6K) - RATTUS NORVEGICUS (RAT), AND ORYCTOLAGUS CUNICULUS (RABBIT), 502 aa.	3.10E-176	11
2125	cg43933478	47	TTTTTTTTTTTTT TTTTTTTTTTTTT[G /T]TGAAGAGATT CCTGTCATTTAA TTA	G	T			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.|pcls:SWISSPROT-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	7.80E-173	12
2126	cg44131752	1527	ACATGTTTCCAC TTAATACCAGAG A[C/gap]CCCCCC CCTTCCCCTCCC CCTTCCC	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
2127	cg44131752	1535	CCACTTAATACC AGAGACCCCCC CC[C/gap]TTCCC CTCCCCCTTCCC CTCCCCCT	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
2128	cg44131752	1604	ATTGCAATAAAA CAAACCTTTCTC T[G/T]CACAAACA CACCAAAGCTTT ATTCA	G	T			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16

2129	cg44000392	245	CTAGACCGATCTCCGGGGAGCCCCG[G/gap]AGTAGGCGAGCGGCGGCCGCCAGCT	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.10E-172	7
2130	cg44000392	265	CCCCGGAGTAGGCGAGCGGCGGCCG[C/gap]CAGCTAGTTGAGCGCACCCCCCGCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2131	cg44000392	266	CCCGGAGTAGGCGAGCGGCGGCCGC[C/gap]AGCTAGTTGAGCGCACCCCCGCCC	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2132	cg44000392	289	GCCAGCTAGTTGAGCGCACCCCCCG[C/G]CCGCCCCAGCGCGCCGCGGCGGGCG	C	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2133	cg44000392	290	CCAGCTAGTTGAGCGCACCCCCCGC[C/G]CGCCCCAGCGCGCCGCGGCGGGCGC	C	G			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2134	cg43291463	1258	GATCAAGAACAAAAAAAATAGCAGC[T/gap]TTTTTTTTCTGTACAGACGTATAG	T	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q25197 PROTEIN-TYROSINE KINASE - HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS), 1477 aa.	6.5E-172	15 (15q25)

2135	cg43291463	1616	CCTTGACTCCAAGCCTGTCCGCCAG[A/G]CTGCTTCGGGGCCCATGGCCACCAG	A	G			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q25197 PROTEIN-TYROSINE KINASE - HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS), 1477 aa.	6.5E-172	15 (15q25)
2136	cg43007055	1516	TTTGTTGGAGTGGTGCCAGGTACTG[G/gap]TTTTGGAGAACTTGTCTACAACCAG	G	gap			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2137	cg43007055	1568	GATTGATTTTAAAGATGTCTTTTTT[T/gap]ATTTTACTTTTTTTTAAGCACCAAA	T	gap			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2138	cg43007055	1583	TGTCTTTTTTTATTTTACTTTTTTT[T/gap]AAGCACCAAATTTTGTTGTTTTTTT	T	gap			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2139	cg43007055	1601	TTTTTTTAAGCACCAAATTTTGTTG[gap/T]TTTTTTTTTTCTCCCCTCCCCACAG	gap	T			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2140	cg43007055	1611	CACCAAATTTTGTTGTTTTTTTTTTT[gap/T]CTCCCCTCCCCACAGATCCCATCTC	gap	T			SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)

2141	cg43007055	1611	CACCAAATTTTG TTGTTTTTTTTTTT[gap/T]CTCCCCTC CCCACAGATCCC ATCTC	gap	T		SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2142	cg43007055	2474	GTCTTTGAGAAT AAAGGAAAAAAA A[gap/A]TCTTCA GATGCAATGGTT TTGTGTA	gap	A		SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2143	cg43007055	350	GTGCCGCTGCC GCTGTTGCCGCC GC[C/gap]GCTGC TGCTGCTGCTCG CCCCGTCG	C	gap		SILENT-NONCODING	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2144	cg43925513	189	TGAATTATTTATT CCTCTCTTCCAT[C/gap]AGATGAG GCTTATCGTGTC AAATCC	C	gap		SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.[pcls:SWISSPROT-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.	1.2E-165	14

2145	cg43925513	346	TGGAAGGACTGTGTTGTGCAGCTGC[A/gap]CATAGCTATAATTTTATAAGTCTGC	A	gap			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.|pcls:SWISSPROT-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.	1.2E-165	14
2146	cg43336176	2028	TGCCCCTCAGTTGAGTGGGCAGGGC[C/gap]GGGGGTGGTCCAGCCCTCGCCCGGC	C	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa.	1.1E-164	19
2147	cg43982923	1494	TCCGACTTCTGTCCGCCCTAGGCCC[C/gap]GGGACCCCCGGCCTCCAGGCTGGGG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2148	cg43982923	1505	TCCGCCCTAGGCCCCGGGACCCCCG[G/gap]CCTCCAGGCTGGGGCCTGGCCTATT	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

2149	cg43982923	1519	CGGGACCCCCG GCCTCCAGGCT GGG[G/gap]CCTG GCCTATTTAAGC CCCCTCTTG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2150	cg43982923	1551	CTATTTAAGCCC CCTCTTGAGAGG G[G/gap]TGAGAC AGTGGGGGGTGC CTGGTGCG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2151	cg43982923	1585	TGGGGGTGCCT GGTGCGCTGTG CTC[C/gap]AGCA GTGCTGGGCCC AGCCGGGGGTG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2152	cg43982923	1600	CGCTGTGCTCCA GCAGTGCTGGG CC[C/gap]AGCCG GGGTGGGGGTGC CTGAGCCCG	C	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2153	cg43982923	1605	TGCTCCAGCAGT GCTGGGCCCAG CC[G/A]GGGTGG GGTGCCTGAGC CCGAATTT	G	A			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

2154	cg43916763	76	ATACTGCGTTCC ATCCCGACCCG GG[G/gap]CCACG GTACTGGGCCCT GTTTCCCC	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSNEW-ID:P24941 CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) - HOMO SAPIENS (HUMAN), 298 aa.|pcls:SWISSPROT-ID:P24941 CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) - HOMO SAPIENS (HUMAN), 298 aa.	1.2E-158	12 (12q13)
2155	cg43921600	115	CTGGCTCTTGGA AATTGAGCGGAG A[G/gap]CGACGC GGTTGTTGTAGC TGCCGTG	G	gap			SILENT-NONCODING	kinase	Human Gene SWISSPROT-ID:P06493 CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1) - HOMO SAPIENS (HUMAN), 297 aa.	2.6E-158	10 (10q21.1)
2156	cg43933460	98	GACGGTTTCTGA GCGTTGGCCTTT G[G/gap]CACGCG CTACCCCCTTTT GCTTTGG	G	gap			SILENT-NONCODING	kinase	Human Gene SPTREMBL-ID:Q63185 EUKARYOTIC INITIATION FACTOR 2A PROTEIN KINASE - RATTUS NORVEGICUS (RAT), 620 aa.	2.3E-155	7
2157	cg43257282	1399	CCCCAGAAAAAG GCCGGGTGACA CC[G/gap]GGGG GCTCCCAGCCC GTGCACCCTG	G	gap			SILENT-NONCODING	kinase	Human Gene Homologous to SPTREMBL-ID:Q15130 CDC2-RELATED KINASE - HOMO SAPIENS (HUMAN), 316 aa.	2.9E-147	16
2158	cg43958362	161	TTTTGAAAAGTC ACAAAAAAGGGT A[C/gap]CCCCAA ACTCAGGTATAC CAAGTAA	C	gap			SILENT-NONCODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP-ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2159	cg43958362	2286	CCCGGAACCGC GGGTCCCAAGG AGC[C/gap]TGCG GAAGGAGTCGG AGCACCAGGA	C	gap			SILENT-NONCODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP-ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12

2160	cg43958362	322	CTCCCGGGAAAC TGAGCTGCGTAT A[A/C]AGAAGTCT GCTTTGGTCCAA AGGAC	A	C			SILENT-NONCODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP-ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2161	cg43958362	716	TCTAGACGTGGT GACTTAAAAAAT G[G/gap]CCTTAA GGCTGCAGAGC CAGCCACC	G	gap			SILENT-NONCODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP-ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2162	cg44016530	214	CATGTTTTTTTTT TTTTTTTTGTTTT[T /A]TAGAGTTTTTTT AACATAAAGTTTT A	T	A			SILENT-NONCODING	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.70E-129	12
2163	cg43265203	982	CAACATCACTGG AAGAAATACCTA T[C/T]GTTAAACC CTGATATACATT CTTAA	C	T			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.|pcls:SWISSPROT-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2164	cg43265203	54	GGATTTATTTTAA TTTTTCAATCTG[A/gap]AAAAAAAA AAACCCAAAACA AAAAA	A	gap			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.|pcls:SWISSPROT-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	

2165	cg43265203	65	AATTTTTCAATCTGAAAAAAAAAAA[A/gap]CCCAAAACAAAAAAAAACAAACTAT	A	gap			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.|pcls:SWISSPROT-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2166	cg43265203	73	ATCTGAAAAAAAAAAAACCCAAAAC[gap/A]AAAAAAAAACAAACTATCCTCATAT	gap	A			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.|pcls:SWISSPROT-ID:P54619 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2167	cg42866488	1761	AGTCGCTCTCATGAAGCCCTTAGGG[gap/G]AGAGCACCTGTTGTGTGCCTGACAC	gap	G			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.|pcls:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2168	cg42866488	2065	TTGGGGAGAGCTGGCAGTGTGCGGA[C/gap]GCTGATAACATTTTCCCAATATTGA	C	gap			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.|pcls:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16

2169	cg42866488	2449	TGGAATTACTGA AAGTCTGTGGCC C[gap/T]AAGAGA GAGACACAAGTG GCCTTAA	gap	T			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.|pcls:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2170	cg42866488	2691	TTTGCAAATAAA GGCTCTGGAAG CA[A/T]AAAAAAA AAAAAAAAAAA AA	A	T			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.|pcls:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2171	cg42866488	2692	TTGCAAATAAAG GCTCTGGAAGCA A[A/T]AAAAAAAA AAAAAAAAAAA	A	T			SILENT-NONCODING	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.|pcls:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2172	cg42925992	133	GGAGGGAGGCG GGGGCACCTG GGG[C/gap]CCGC CATGAACCCCGG CTTCGATTT	C	gap			SILENT-NONCODING	kinase	Human Gene Homologous to SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	5.10E-105	
2173	cg43918705	1032	CTCACCAAACGA AGGGTATCAGCT A[T/gap]TTTTTTT TTAAATTCAAAAA GAATA	T	gap			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.|pcls:SPTREMBL-ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1

2174	cg43918705	1152	CAACATTTTAGG ATTTAGGGATAC C[T/C]GCTTCCTC TTTTTCTTGCAA GTTTT	T	C			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.|pcls:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2175	cg43918705	1728	ATCTAGTTAAATT TCCCATTTGTAT[T/A]TTATTTTCTT GAATACTTTTTTC AT	T	A			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.|pcls:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2176	cg43918705	2392	AGGCCAGCAAAT ACAGAGGTGGTT T[G/A]ATCAAACA GCTCTAGTATGA AGCAA	G	A			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.|pcls:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1

2177	cg43918705	2839	ATTCAGTGATGT TGGATGTATATC A[A/G]TTATTTAG TAAATAATCTCAA TAAA	A	G			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.|pdb:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2178	cg43965859	147	GCTGCGCTCAG GCCAGGAGGAC CTC[T/G]AATCAG GACGGGGTGGG GCGGGGCT	T	G			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P00568 ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE) - HOMO SAPIENS (HUMAN), 194 aa.	2.40E-98	9 (9q34.1)
2179	cg43965859	73	TTTAGTGCTCAG CTGTCCATGAAA A[C/A]AGGATAAG CGGCTTCCTCCG TCTGT	C	A			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P00568 ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE) - HOMO SAPIENS (HUMAN), 194 aa.	2.40E-98	9 (9q34.1)
2180	cg43952004	165	GGGAGTTCTTGA GGCTGAGTGCG TA[gap/G]CTTCA AATCCAGCACTA ATTCCTCA	gap	G			SILENT-NONCODING	kinase	Human Gene Similar to TREMBLNEW-ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14
2181	cg43952004	229	GGTCTTCATAGA TTGGTGGCTTGA G[C/gap]CCTGCA ATTAATTATAATC CCTTGC	C	gap			SILENT-NONCODING	kinase	Human Gene Similar to TREMBLNEW-ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14
2182	cg43952004	231	TCTTCATAGATT GGTGGCTTGAG CC[C/gap]TGCAA TTAATTATAATCC CTTGCCC	C	gap			SILENT-NONCODING	kinase	Human Gene Similar to TREMBLNEW-ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14

2183	cg43970923	1814	CCCAGCTATCCCCGCTCTGACCTTG[gap/G]ATTTTCATTCTTATGTTTTTCTCTT	gap	G			SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:P97841 GUANYLATE KINASE ASSOCIATED PROTEIN - RATTUS NORVEGICUS (RAT), 666 aa.	1.40E-92	
2184	cg44924345	157	TTTTGTCGTTCCAAAGTACAAAAAG[gap/A]AAAAAAAATCAAAGGCATTTCATC	gap	A			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P52623 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - MUS MUSCULUS (MOUSE), 260 aa (fragment).	7.10E-92	1
2185	cg44924345	166	TCCAAAGTACAAAAAGAAAAAAAAA[gap/A]TCAAAGGCATTTCATCTCCATGGTG	gap	A			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P52623 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - MUS MUSCULUS (MOUSE), 260 aa (fragment).	7.10E-92	1
2186	cg43966625	652	CACAGCGGCGGGGAGCGGGCGGTGG[A/G]GGGGGCGGTGCTGGGCCCAGGGCCG	A	G			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.|pcls:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-89	17
2187	cg43266014	219	ACGTGGAGGATCACTCGGTGGATAA[A/T]TAAGGATAAGTTGAGCGAGGGCGTG	A	T			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P23919 THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE) - HOMO SAPIENS (HUMAN), 212 aa.	1.00E-87	
2188	cg43983647	440	AAATTCCTTCTCTTCTCCTGAACTG[C/T]TGACTTTCAAAAATTCACAGAATGA	C	T			SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q62920 PROTEIN KINASE C-BINDING PROTEIN ENIGMA - RATTUS NORVEGICUS (RAT), 520 aa (fragment).	1.10E-86	4

2189	cg43919577	1068	ACAAGCAGTGCA CAGTGGGCCGG CA[G/gap]GTACT TAAGTACCTTAT CCTAATCC	G	gap		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q63835 PHOSPHATIDYLINOSITOL 4-KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2190	cg43919577	1069	CAAGCAGTGCAC AGTGGGCCGGC AG[G/gap]TACTT AAGTACCTTATC CTAATCCT	G	gap		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q63835 PHOSPHATIDYLINOSITOL 4-KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2191	cg43919577	117	GACTTTACATTTA CAAGTAGAAACA[A/G]CATGTGTTA TCTGTGGGTAAG GTAG	A	G		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q63835 PHOSPHATIDYLINOSITOL 4-KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2192	cg43919577	416	TTAAGAACAGCA TTCCTTTTGGAC A[G/A]TATGTCAT AGACCCAATTTT TAATA	G	A		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q63835 PHOSPHATIDYLINOSITOL 4-KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2193	cg43971367	2030	GAGCGGCAGGA GAACGTCTGGAG GC[G/gap]GCACT GTTGCCGATCCG GGTCTGGA	G	gap		SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P54352 ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 517 aa.	1.60E-75	
2194	cg43980968	1675	CCCAGTGCCCAC AGGTGGCAGGA GC[C/gap]TGTCC AGGGACTCTGCA TTGCTGCC	C	gap		SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P27515 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 501 aa.	9.50E-75	

2195	cg43984445	247	AGGGAGCCCAG ATCACAGCCTGA AC[A/T]TCATGGT ATTGGTTACAGA TTCTTT	A	T		SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:Q16854 DEOXYGUANOSINE KINASE PRECURSOR (EC 2.7.1.113) (DGUOK) - HOMO SAPIENS (HUMAN), 277 aa.lpcls:SPTREMBL-ID:Q16854 DEOXYGUANOSINE KINASE (EC 2.7.1.113) - HOMO SAPIENS (HUMAN), 277 aa.	8.70E-73	2
2196	cg43246312	890	CGTGAATGGCCA GAGCTACTCTTC A[A/C]TTGCTGAA CAATGTCAAAAA GAATT	A	C		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q90269 INTRACELLULAR TYROSINE KINASE DOMAINS OF PLATELET-DERIVED GROWTH FACTOR RECEPTOR SUBTYPE ALPHA - BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO), 457 aa (fragment).	4.20E-62	11
2197	cg43246312	939	TTGACACTTGCT GAACAAATCTTT A[A/C]AAGTCAGA ACTTCTGATGGA TTAAA	A	C		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q90269 INTRACELLULAR TYROSINE KINASE DOMAINS OF PLATELET-DERIVED GROWTH FACTOR RECEPTOR SUBTYPE ALPHA - BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO), 457 aa (fragment).	4.20E-62	11
2198	cg43968142	201	GCCCCTGACCCA GCCCCCTTAAGC C[A/G]GCCAGGC AGGGTCCCCGG ACACCCT	A	G		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:O09132 A6 PROTEIN TYROSINE KINASE HOMOLOG - MUS MUSCULUS (MOUSE), 350 aa.	3.00E-61	3
2199	cg43968142	396	GTGGCAGGGAG CGGAAGGTGGG CAG[C/gap]CCCA CAGTCCACACGT GGCCGGCCC	C	gap		SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:O09132 A6 PROTEIN TYROSINE KINASE HOMOLOG - MUS MUSCULUS (MOUSE), 350 aa.	3.00E-61	3

2200	cg43918784	361	AAACGGGTAACT GTACCTGTTAAA T[C/A]TCCTGGTT GGCAACTTTTAA AATCT	C	A			SILENT-NONCODING	kinase	Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2201	cg43918784	509	TCCATAAATAATA TTAACATTTTCA[A/G]TGTAGAAAT CTTGAAGTTCTA AAGG	A	G			SILENT-NONCODING	kinase	Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2202	cg43918784	706	AACTCTTCGGTT ACAATGGATTCC T[C/T]GGTTTCTG ATTTGTCGGTAT CCGAA	C	T			SILENT-NONCODING	kinase	Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2203	cg43979971	1998	TAAAAAAATAATT TTTTAAAACTTA[A/C]AACACTACG AGATCTGATTTA TTCT	A	C			SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2204	cg43979971	285	GCCGCGACAGC AGCGCCGGCCC CGG[gap/C]AGCT CCCGCGGCCCC GGCCCCGGCC	gap	C			SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2205	cg43979971	321	GCCCCGGCCCC GGCCCCGGCCC CGG[C/gap]CCCG GCGGCACAGGC TGTCGGCTGG	C	gap			SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2206	cg43979971	324	CCGGCCCCGGC CCCGGCCCCGG CCC[C/gap]GGCG GCACAGGCTGTC GGCTGGCCC	C	gap			SILENT-NONCODING	kinase	Human Gene Similar to SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2

2207	cg43928048	1310	CTAAACTATATATGTATTTTTTCCA[T/C]AGGAAAGCACAAGGAGAAGACAGAA	T	C			SILENT-NONCODING	kinase	Human Gene Similar to SWISSPROT-ID:P20505 30 KD PROTEIN KINASE HOMOLOG (EC 2.7.1.-) (PROTEIN B1) - VACCINIA VIRUS (STRAIN COPENHAGEN), 300 aa.	5.30E-55	
2208	cg43105476	234	AGATGTTGCTTAAATATATTCATAA[G/A]CCTGTTGTAAGATTTTCACTTATGC	G	A			SILENT-NONCODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
2209	cg42714770	146	GTCATGAAGTCGACAGCTTCCGGAG[G/gap]CTGCGAGGCTCGCAAGAAATGCCCA	G	gap			SILENT-NONCODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)
2210	cg42714770	317	GACATTTACGGTAGTGGGGGAAGGC[A/T]TATATCTACGTTAAAAGGCAGGACA	A	T			SILENT-NONCODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)
2211	cg42714770	450	TCGGTGACTGATGATCTAAGTTTCC[G/C]GAGGTTTCTCAGAGCCTCTCTGGTT	G	C			SILENT-NONCODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)
2212	cg42714770	454	TGACTGATGATCTAAGTTTCCGGAG[G/gap]TTTCTCAGAGCCTCTCTGGTTCTTT	G	gap			SILENT-NONCODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	1.40E-79	9 (9p21)

2213	cg42714751	61	AGATGGGCAGG GGGCGGTGCGT GGG[G/T]CCCAG TCTGCAGTTAAG GGGGCAGG	G	T			SILENT-NONCODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	2.60E-53	9 (9p21)
2214	cg44021336	191	ACACACCTGTGG GGCAGCTGAACT A[G/A]AAAGAAG GATGCCCAGGAT AGCTAT	G	A			SILENT-NONCODING	kinasereceptor	Human Gene SWISSNEW-ID:P35590 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1138 aa.|pdb:SWISSPROT-ID:P35590 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1138 aa.	0.00E+00	1
2215	cg43241731	301	GAATCTGCGCCC CAGAGAGTCCC GG[G/gap]AGCGC CGCCGGTCGGT GCCCGGCGC	G	gap			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:Q16620 BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B) - HOMO SAPIENS (HUMAN), 822 aa.	0.00E+00	9
2216	cg43917080	209	GATACACCGGGT GTGGGATTTACA A[A/C]TAGGACCA ACAATGTGTGCG GGGCA	A	C			SILENT-NONCODING	kinasereceptor	Human Gene SPTREMBL-ID:Q01974 PROTEIN-TYROSINE KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 943 aa.	0.00E+00	9
2217	cg43917080	232	AAATAGGACCAA CAATGTGTGCGG G[G/gap]CACAGA CGGCTGCCTGT GGGTCTGT	G	gap			SILENT-NONCODING	kinasereceptor	Human Gene SPTREMBL-ID:Q01974 PROTEIN-TYROSINE KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 943 aa.	0.00E+00	9
2218	cg44021449	3336	CACACAGTAGCT GTTAGCCCACAG G[C/gap]AGAGGG CATCGGGGCCAT TTGGCCG	C	gap			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15

2219	cg44021449	3359	GGCAGAGGGCA TCGGGGCCATTT GG[C/gap]CGGCT CTGGTGGCCACT GAGCTGGC	C	gap			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15
2220	cg44021449	4345	CTGTTAGGGACA TTTCCAAGCTGT T[A/G]GTTGCTGT TTAAAATAGAAAT AAAA	A	G			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15
2221	cg43322545	2964	GGGGAAAACTCC ACCTTCCCACTT T[C/T]CCACCCCA CGCCTTATCCCC ACTTG	C	T			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSNEW-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.|pcls:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0.00E+00	19 (19q13.1)
2222	cg44024023	641	CCTGCTCCAGG GATGCTGGGAC GTG[gap/G]CGGT GCCTGCTAAGTG CTCAGCTGT	gap	G			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29317 EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 976 aa.	0.00E+00	
2223	cg44024023	669	GTGCCTGCTAAG TGCTCAGCTGTG T[G/gap]CGTCTC GCAGGGAAAGA GGGCCCAG	G	gap			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29317 EPHRIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 976 aa.	0.00E+00	

2224	cg44025829	1915	AGGAAGATTTGACGTTGTTGTCATT[G/T]TCCAGCTGGGACCTAATGCTGGCCT	G	T			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:Q04771 ACTIVIN RECEPTOR TYPE I PRECURSOR (EC 2.7.1.-) (ACTR-I) (SERINE/THREONINE-PROTEIN KINASE RECEPTOR R1) (SKR1) (ACTIVIN RECEPTOR-LIKE KINASE 2) (ALK-2) (TGF-B SUPERFAMILY RECEPTOR TYPE I) (TSR-I) - HOMO SAPIENS (HUMAN), 509 aa.	7.90E-283	2
2225	cg43263845	277	GAAGACCCAGGGAACTGGATATCTA[G/T]CGAGAACTTCCTCCGGATTCCCCGG	G	T			SILENT-NONCODING	kinasereceptor	Human Gene TREMBLNEW-ID:G247985 ACTIVIN RECEPTOR, ACTRIIB=TRANSMEMBRANE PROTEIN SERINE KINASE - XENOPUS LAEVIS, 510 aa.	3.30E-204	2
2226	cg43954819	1423	GTGAGCATCCTGGCAGGTGCCCCAG[G/T]ATGCCACGCCTGGAAGGGCCGGCTT	G	T			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2227	cg43954819	1573	GTCTCACTCGTTCTGTTACCCAGGG[C/gap]TCTGCAGCACCTCACCTGAGACCTC	C	gap			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2228	cg43954819	1808	CTGGGGAAAGGGCTGGCTGCAATTG[C/gap]AGCTCACTGCTGCTGCCTCTGAAAC	C	gap			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2229	cg43954819	2795	TGCAAAAATAACCAAGTCCTCCGAA[G/gap]GCATCTCACGGAACCGTAGACTAGG	G	gap			SILENT-NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13

2230	cg43954819	2796	GCAAAAATAACC AAGTCCTCCGAA G[G/gap]CATCTC ACGGAACCGTAG ACTAGGA	G	gap			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2231	cg43954819	46	CGGAAGGCGCG GAGCTGGGAGT GGC[A/T]CAGCC ATGGCTGTGAGA AGGGACTC	A	T			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2232	cg43954819	48	GAAGGCGCGGA GCTGGGAGTGG CAC[A/C]GCCAT GGCTGTGAGAA GGGACTCCG	A	C			SILENT-NONCODING	kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2233	cg43999555	1630	AGGCCCAGCTG CCTTGGGCTGG GGC[C/gap]TGCG GAGGGGAAGCC CACCCACAAT	C	gap			SILENT-NONCODING	kinaserec eptor	Human Gene Similar to SWISSPROT-ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa.|pcls:SPTREMBL-ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.20E-99	11
2234	cg43980494	897	CTCACAAGTCCC TGGGAAGACAG GG[C/T]ATGGGC TTACAGAGAGGA GAGGGGG	C	T			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2235	cg43980494	1446	TGGTCCGAAATA TAAGCCGAGCTC A[G/T]CATCTTGC CACACACGTGAC ATGGC	G	T			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16

2236	cg43980494	376	GGGGACACAGG AACACGATGACA TG[G/gap]CCAGG GCCACAACTTCT TCTGTCGT	G	gap			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2237	cg43980494	383	CAGGAACACGAT GACATGGCCAG GG[C/gap]CACAA CTTCTTCTGTCG TGGGGAAG	C	gap			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2238	cg43980494	384	AGGAACACGATG ACATGGCCAGG GC[C/gap]ACAAC TTCTTCTGTCGT GGGGAAGA	C	gap			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2239	cg43980494	481	AGGGGGACACT GGCTGCATTCCC CC[G/C]CCCCCA GGAAGCACCTCT AGGCCCT	G	C			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2240	cg43980494	489	ACTGGCTGCATT CCCCCGCCCCC AG[G/gap]AAGCA CCTCTAGGCCCT GGACCCCT	G	gap			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2241	cg43980494	515	AAGCACCTCTAG GCCCTGGACCC CT[C/G]GCTCAC CCTGGCCCCTAA GACTCCA	C	G			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2242	cg43980494	559	GACTCCATCTCT TCTCTGCCTCTG G[C/gap]CCTCCT GGCTCTTCCTCC TGCTCCC	C	gap			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16

2243	cg43980494	648	GTTCAGGGCCTG ACCCCAACCCCC C[gap/G]ATACCA CCTTATGAAGGT ACAACCT	gap	G			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2244	cg43980494	768	TCCTTCCTCTCC TCCCTCCCCCTG G[A/gap]AAAAAA AAAAAAAGGAAA AGAAAGC	A	gap			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2245	cg43980494	781	CCTCCCCCTGGA AAAAAAAAAAA A[gap/A]GGAAAA GAAAGCACCAAC TCCCCGG	gap	A			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2246	cg43925424	232	GCGGGGCGGTA GCTCCGGCGCC CCT[C/A]GCTGGT GACTGCTGCGC CGTGCCTC	C	A			SILENT-NONCODING	kinesin	Human Gene SWISSPROT-ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	1.90E-304	14
2247	cg43987378	2380	TTTTTTTAAATA AAGGTTTTATTA[G/C]CATTTGCCC AAGAAGGCAGAT ACTT	G	C			SILENT-NONCODING	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.50E-254	6
2248	cg43068603	1956	AAAATCCATTTC AAATTTATTGATG [G/C]ATTCATGTT GTTCTTCTTTTAT TTT	G	C			SILENT-NONCODING	kinesin	Human Gene Similar to SWISSPROT-ID:P33174 KINESIN-LIKE PROTEIN KIF4 - MUS MUSCULUS (MOUSE), 1231 aa.	1.70E-79	4 (4q24)
2249	cg44002977	231	GCTAGCTACTCT AGAGGACCACA GG[G/A]TGCAGA GAGGGTGTCCT GAGGGTCC	G	A			SILENT-NONCODING	kinesin	Human Gene Similar to SWISSPROT-ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6

2250	cg44002977	406	TGTGAGGGCTGTGGGGGTGGGGGGA[C/gap]CCAGCAGACCTGGGGGCCGGGTTGA	C	gap			SILENT-NONCODING	kinesin	Human Gene Similar to SWISSPROT-ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6
2251	cg43946310	3902	ACTCCTTGCTTCCTGATGCTGGGCA[A/gap]TGAGGCAGATAGCACTGGGTGTGAG	A	gap			SILENT-NONCODING	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2252	cg43946310	4427	AGATTGCATTTTTATTAAAGCATTT[C/G]CTACCAGCAAAGCAAATGTTGGGAA	C	G			SILENT-NONCODING	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2253	cg43946310	4440	ATTAAAGCATTTCCTACCAGCAAAG[C/G]AAATGTTGGGAAAGTATTTACTTTT	C	G			SILENT-NONCODING	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2254	cg43983535	143	GAATTAGCACCATCTGAATACAGA A[G/A]GAATTCTATGTACATGCACAAATTA	G	A			SILENT-NONCODING	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0.00E+00	6 (6q22)
2255	cg44009224	5282	CTCCCCAGCTCGAGATCATTCTTCA[C/A]TCAGGACACAAACCAGACAGGTTTA	C	A			SILENT-NONCODING	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	

2256	cg4358558	283	AGGTTTAGATTC TTTTTTTTTTTT[gap/T]AATCTGCC CCTTTCAGATTA TATCA	gap	T		SILENT-NONCODING	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.|pcls:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)

2257	cg43958558	283	AGGTTTAGATTC TTTTTTTTTTTT[gap/T]AATCTGCC CCTTTCAGATTA TATCA	gap	T		SILENT-NONCODING	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.|pdb:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
2258	cg43970746	127	GGGAGGAGGGG AAGTGAGGCCC CAG[C/gap]CCCA CAACCCCTCCCC GCCCACCCC	C	gap		SILENT-NONCODING	MHC	Human Gene SWISSPROT-ID:P48634 LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) - HOMO SAPIENS (HUMAN), 2142 aa.	0.00E+00	3
2259	cg43921887	335	CATTCAGCATGA TTCCACCTGGGC A[T/C]GAGCTGG AAAAGAGCTCAG TCTTCA	T	C		SILENT-NONCODING	MHC	Human Gene SWISSPROT-ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	0.00E+00	14
2260	cg43298284	1921	TGAGTTGCACAG CTATGAAGGCTG T[G/A]CACTGCAC GAATGGAAGAG GCACCT	G	A		SILENT-NONCODING	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6

2261	cg43298284	2363	CGGTGGCTCGC GCCTGTGGTCCC AG[C/gap]ACTTT GGGAGGCCAAA GCGGTGCTG	C	gap			SILENT-NONCODING	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2262	cg43298284	2394	GGGAGGCCAAA GCGGTGCTGAG ATT[G/A]CAGGTG TGAGCCACCCTG CCCAGCC	G	A			SILENT-NONCODING	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2263	cg43298284	2506	ACTTGGCTGCAT AAATGTGGTACA A[G/C]CATTCTGT CTTGAAGGGCAG GTGCT	G	C			SILENT-NONCODING	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2264	cg42479188	1420	TCCCCTGAGACC TTACTCCTTCCA G[C/T]CCCAAATC ATTTACTTTTCTG TGGT	C	T			SILENT-NONCODING	MHC	Human Gene Homologous to SWISSPROT-ID:P13765 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DO BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 273 aa.	3.40E-147	6 (6p21.3)
2265	cg43966144	99	CACTCATTTGGG GGGTCAAGGGA CC[C/gap]GGGCA ATATAGTATTCT GCTCAGTG	C	gap			SILENT-NONCODING	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147	6 (6p21.3)
2266	cg39425214	678	GGCAGCGGGAC CCGCCCAGACC CTC[C/G]ACCCG GGAGAGTCCCA GGCGCCTTT	C	G			SILENT-NONCODING	MHC	Human Gene Similar to SWISSPROT-ID:P16215 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN PRECURSOR - PAN TROGLODYTES (CHIMPANZEE), 346 aa.	4.70E-55	
2267	cg42928872	3016	GACAGGGGTTC CTTCTGGGCATT AC[A/G]TCGCATA GAAATCAATAAT TTGTGG	A	G			SILENT-NONCODING	misc_channel	Human Gene TREMBLNEW-ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	11

2268	cg42928872	3073	GGATCTGTGTTTTAATGAGTTTCAC[A/G]GTGTGATTTTGATTATTAATTGTGC	A	G			SILENT-NONCODING	misc_channel	Human Gene TREMBLNEW-ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0	11
2269	cg43984759	158	CGTCGAGTGACAGCGGCCTGGGGGG[G/gap]CAGGGGGGGCGGGGGCGGCCGGATC	G	gap			SILENT-NONCODING	misc_channel	Human Gene SPTREMBL-ID:Q14193 H-DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2270	cg43984759	3297	GCTACAGGGAATGATTGGTCATGGG[G/gap]AAGTCTCTGCGCCATAAGCCACGAT	G	gap			SILENT-NONCODING	misc_channel	Human Gene SPTREMBL-ID:Q14193 H-DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2271	cg43984759	3324	AGTCTCTGCGCCATAAGCCACGATC[C/A]CAGCGCAAAACCCTTACTCAAATGT	C	A			SILENT-NONCODING	misc_channel	Human Gene SPTREMBL-ID:Q14193 H-DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2272	cg43984759	3379	ATTGACTTCGGTATTTCATAGTACC[T/C]GAGATTTTATTTTGAGATACCATCA	T	C			SILENT-NONCODING	misc_channel	Human Gene SPTREMBL-ID:Q14193 H-DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2273	cg43984759	3388	GGTATTTCATAGTACCTGAGATTTT[A/T]TTTTGAGATACCATCAGGGTGAGTT	A	T			SILENT-NONCODING	misc_channel	Human Gene SPTREMBL-ID:Q14193 H-DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20

2274	cg43957213	130	GGCAAGATTCAGTCCCTGACCGCAA[G/gap]GCACTTACAGTCTAGTTGGGAAGGG	G	gap			SILENT-NONCODING	misc_channel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.|pdb:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.|pdb:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa.	0	1 (1p36.1)

2275	cg43957213	131	GCAAGATTCAGTCCCTGACCGCAAG[G/gap]CACTTACAGTCTAGTTGGGAAGGGA	G	gap		SILENT-NONCODING	misc_channel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.|pcis:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.|pcis:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa	0	1 (1p36.1)
2276	cg42684570	221	AACCTAAAAGCAAAGTTGTGAAAGA[G/A]AAGCAGAATTCCAAAGTCCCTTATT	G	A		SILENT-NONCODING	misc_channel	Human Gene SWISSPROT-ID:P46098 5-HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN-GATED ION CHANNEL RECEPTOR) - HOMO SAPIENS (HUMAN), 478 aa.	1.8E-260	11 (11q23.1)
2277	cg40367355	1773	AGGGCAATTGGAATAATGTCCTGTT[A/G]GATAAACAGACATTTAGCAATGCTG	A	G		SILENT-NONCODING	misc_channel	Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.10E-199	21
2278	cg44963814	1142	GGGGCCAGCCCCTCCCCGCCTCCTC[C/T]CTGCCTGGCGGCAGGGGTCGCGATG	C	T		SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcis:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)

2279	cg44963814	1152	CCTCCCCGCCTC CTCCCTGCCTGG C[G/gap]GCAGGG GTCGCGATGATG GGCTGGA	G	gap			SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcls:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2280	cg44963814	1220	TTCTGGGACCCA CTCCGACTCCCC C[gap/C]TCCCCG GCATCATTTCCC CTCCCGC	gap	C			SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcls:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2281	cg44963814	1285	CCTGGGGTCCC CCCTCCCTGTAA TG[C/G]ACTCCTG CCCCGGCCCAA CCTCGCC	C	G			SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcls:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2282	cg44963814	797	CCGCCTCAAGGA AGAGCCAGCCG TA[A/gap]TGGGG ACTCTCCAGGCA CCGCCTGC	A	gap			SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcls:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)

2283	cg44963814	805	AGGAAGAGCCA GCCGTAATGGG GAC[T/C]CTCCAG GCACCGCCTGC CCCCAGCG	T	C			SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcls:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2284	cg44963814	854	GTGGGGGTGGC CACTCCTGGGCC CC[gap/C]AGAAA GCCTCAGAGTCC TGCCGACG	gap	C			SILENT-NONCODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.|pcls:TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2285	cg43328088	392	TGCTTGAGGAAG GTCTTGAGAAAA C[G/C]CTCACTCC CTCTAAACTTTTA GCTT	G	C			SILENT-NONCODING	misc_channel	Human Gene Similar to SWISSPROT-ID:P35526 CHLORINE CHANNEL PROTEIN P64 - BOS TAURUS (BOVINE), 437 aa.	2.70E-99	1
2286	cg43309398	221	GCTCTTGGTCCA GCTGGTCGCGG GG[G/gap]CGCTG CGGTCTAGCCG GGCGCGGCG	G	gap			SILENT-NONCODING	misc_channel	Human Gene Similar to SPTREMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.10E-67	15 (15q24)
2287	cg43309398	236	GGTCGCGGGGG CGCTGCGGTCTA GC[C/gap]GGGCG CGGCGGGCGGC GCGCAGAGA	C	gap			SILENT-NONCODING	misc_channel	Human Gene Similar to SPTREMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.10E-67	15 (15q24)
2288	cg43978512	1658	ATCCTTCCCCCG CATGTTCATAGA C[G/A]GACAGAC TTCTACTTTCAGT CGCTA	G	A			SILENT-NONCODING	misc_channel	Human Gene Similar to SWISSPROT-ID:Q15700 CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN 110) - HOMO SAPIENS (HUMAN), 870 aa.	6.20E-53	10

2289	cg43978512	1702	GTCGCTAGAAA GAGCTGAGTCTG G[C/T]GTCCCCTC AGGCGGCCAGC TGCAGT	C	T		SILENT-NONCODING	misc_channel	Human Gene Similar to SWISSPROT-ID:Q15700 CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) - HOMO SAPIENS (HUMAN), 870 aa.	6.20E-53	10
2290	cg43013507	1808	TCGCACGCCCG AGGGCCGGCCT CCG[G/gap]TCCC GCTTCCAGTTTC CTTGAAGCG	G	gap		SILENT-NONCODING	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2291	cg43013507	1987	GATTCAAGACAG TCTTTTGTAACT G[G/gap]CACACG CCCCACGCCTTC CTCTATA	G	gap		SILENT-NONCODING	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2292	cg43013507	2037	AACCCCCAGAGA CAGGCTGGGGC AG[C/gap]GCCAA GGCGGTCTCGC GCGGGACTT	C	gap		SILENT-NONCODING	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2293	cg43013507	2089	TACAGCAGTGTC TTATCCAGCAGC C[gap/G]ATTGGA TGTAACGTTTTG CTTTGGG	gap	G		SILENT-NONCODING	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI- C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2294	cg44929972	1659	TTAAACTCTAGA CACAGTTTTTAT C[T/C]TGGATTAA CTTAGATAACTTT TGTA	T	C		SILENT-NONCODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7

2295	cg44929972	2199	GTAACACTGATTTTATCTGCTGTAT[G/A]AGACTTTGTGCATTTTACTTTGAAA	G	A			SILENT-NONCODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7
2296	cg43940300	227	CTTTGTCTTTTCTGTCAGAATAGCT[T/C]ACAAACATACTACTACTATTTATTT	T	C			SILENT-NONCODING	ngf	Human Gene Similar to SWISSNEW-ID:P78543 BTG2 PROTEIN PRECURSOR (NGF-INDUCIBLE ANTI-PROLIFERATIVE PROTEIN PC3) - HOMO SAPIENS (HUMAN), 158 aa.|pcls:SWISSPROT-ID:P78543 BTG2 PROTEIN PRECURSOR (NGF-INDUCIBLE ANTI-PROLIFERATIVE PROTEIN PC3) - HOMO SAPIENS (HUMAN), 158 aa.|pcls:SPTREMBL-ID:P78543 NGF-INDUCIBLE PC3 ANTI-PROLIFERATIVE PROTEIN - HOMO SAPIENS (HUMAN), 158 aa.	3.10E-82	1
2297	cg44022292	2240	ATGGTTGCCATGATCTACCGCTTTT[G/gap]CGCCCCTGCTGACTCCGGCGTCGGG	G	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q15625 STEROID RECEPTOR (TR2-11) - HOMO SAPIENS (HUMAN), 603 aa.	0.00E+00	12
2298	cg43971768	182	TAAGAAGAAAGAGAAATGGTTAAGT[A/G]CTTAAACTGTCCACTGACACCTGCT	A	G			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2299	cg43971768	23	TTTTTTTTTTGTTCAGAGCAAA[G/T]TCATTTTTATTGTAATGAAATTTTA	G	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2300	cg43971768	277	TTGTTAGATGAAGCAAGCCGTCCTG[C/T]TCCCGCACAGCCTGTGAAACCTCCA	C	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15

2301	cg43971768	330	TTGCCACTTTCA AGGTCAGTGCCC C[A/G]CAGACCC TGGCCTGTTGTT GACCAT	A	G			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2302	cg43971768	343	GGTCAGTGCCC CACAGACCCTGG CC[T/C]GTTGTTG ACCATAACACTA GCTTTG	T	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2303	cg43991048	204	TAATATTTTTTCA GTGCTACTAATG[gap/A]AAAAAAAA AATTAAAGCCTG CACTG	gap	A			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO-REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
2304	cg43991048	214	TCAGTGCTACTA ATGAAAAAAAAA A[gap/A]TTAAAG CCTGCACTGGAA ATTTACA	gap	A			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO-REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
2305	cg43921419	2593	AACCCCGGCCAT CCATCACAAAGG C[gap/C]AACCTG GGAGAGTAACTA TTTTGGG	gap	C			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0.00E+00	19
2306	cg43921419	3208	ACAATCGGCCCA TCACCGAGCCCC C[C/gap]GGCGCC AGGCCCAGCTC CCCCTCTG	C	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0.00E+00	19
2307	cg43249083	282	TTTGCACCGGGA GCTCCAGATTCG C[C/T]ACCCCGC AGCGCTGCGGA GCCGGCA	C	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	17 (17q11.2)

2308	cg43992723	5608	TGTCTTTCAAA GACACCTGCCTT A[gap/G]TGCAAG GGGAAACCTGTG AAAGCTG	gap	G			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0	4 (4q31.1)
2309	cg43992723	5636	CAAGGGGAAAC CTGTGAAAGCTG CA[G/C]TCAGAG GGAGGAGTTTTT CTTACAT	G	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2310	cg43992723	5651	GAAAGCTGCAGT CAGAGGGAGGA GT[T/C]TTTCTTA CATAATTTGCAA TTTCAG	T	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2311	cg43992723	5848	GTTCAGACTTAG TTTTTATAAAATG [G/A]GAATTCTGA CTTACTTAACCA GGTT	G	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2312	cg43992723	6085	TGGTACAGTTCA TAATTCACCAAA A[gap/A]GTTCATA TAATTTAAAGAAA CACTA	gap	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2313	cg43992723	6102	TCACCAAAAGTT CATATAATTTAAA [G/A]AAACACTAA ATTAGTTTAAAAT GAA	G	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2314	cg42507196	172	TTCGTCCTGGGA CTGCACTTGCTC C[C/gap]GTCGGG TCGCCCGGCTTC ACCGGAC	C	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:P03372 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.|pcls:SWISSPROT-ID:P03372 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.	0.00E+00	6 (6q25.1)

2315	cg43961967	2265	AAGACCACCTTC CCTTCCTCAGCA G[G/gap]CCAAAC ATGGCCAGACTC CCTTGCT	G	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2316	cg43961967	2383	TCCTTTGAGGCC CCAACTCAAGTG T[gap/G]CACCTC CTTCCCCAGCTC CCCCAGG	gap	G			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2317	cg43961967	2414	CTTCCCCAGCTC CCCCAGGCAGA AA[gap/A]TAGTT GTCTGTGCTTCC TTGGTTCA	gap	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2318	cg43961967	2464	TGCTTCTACTGT GACACTTATCTC A[gap/G]CTGTTTT ATAATTAGTCGG GCATGA	gap	G			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2319	cg43961967	455	TGCCACTCCCTG GCCCCTCCCACC G[G/C]CCGCCCC CCTTGGGGCGG AGGGCAT	G	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2320	cg43961967	469	CCCTCCCACCG GCCGCCCCCCTT GG[G/C]GCGGAG GGCATGGTGTGA AAGGCCA	G	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2321	cg43961967	474	CCACCGGCCGC CCCCCTTGGGG CGG[A/gap]GGGC ATGGTGTGAAAG GCCAAGTGC	A	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)

2322	cg43961967	476	ACCGGCCGCCC CCTTGGGGCG GAG[G/C]GCATG GTGTGAAAGGCC AAGTGCTG	G	C		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2323	cg43961967	532	GGTATCATGGGT GCTGTGCCCTAG G[G/gap]CCTGGG TGGCAGGGGGT GGGTGGCC	G	gap		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2324	cg43917579	1583	CTGCCTGGCCTG TTTGGACTTTGG G[G/gap]CACAGC CTGTCACTGCTC TGCCTAA	G	gap		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2325	cg43917579	1745	CGCCTCCCCACC GGGCTCTCAGG AC[A/G]CCCTGC CACACCCCACG GGGCTTGG	A	G		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2326	cg43917579	4479	TCCCCGTGGGG CACCCAGGAGG GCC[C/gap]TGCC GGAATGTGCAGC CTGTGGGTA	C	gap		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2327	cg43917579	4527	GTAGTCGGCTG GTGTCCCTGTCG TG[G/C]AGCTGG GGTGCGTGATCT GGTGCTC	G	C		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2328	cg43917579	50	GCCCGCCGCCC GCTGCCTGCGC CGC[A/C]GGCCG GGGATGAGTTAG TCGCAGAC	A	C		SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9

2329	cg43917579	4951	GCATCTGGAAAG GTAAAAAAAAA A[A/gap]TCTATTT TTGTACAAATGT AATTTT	A	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2330	cg43917579	58	CCCGCTGCCTG CGCCGCAGGCC GGG[G/C]ATGAG TTAGTCGCAGAC AAGGACAC	G	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2331	cg43917579	77	GCCGGGGATGA GTTAGTCGCAGA CA[A/T]GGACACC AAACATTTCCTG CCGCTC	A	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR-ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2332	cg43987181	253	CACACAAAAAG TGCATCTAAATG A[T/gap]TTTTTTT TTTAAAAAACAAT GTCTT	T	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.|pcls:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

2333	cg43987181	2434	GAGTTCACTGGG ACTCTTCCCTCC T[C/T]GGCGTGG CGTCATACGTGG CCCTCA	C	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.|pdb:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6
2334	cg43987181	264	GTGCATCTAAAT GATTTTTTTTTTT[A/T]AAAAACAAT GTCTTTAATTCCT CAT	A	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.|pdb:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

2335	cg43987181	747	TTTCATAAAAAA GACAAAAGCATA A[T/A]TGAGAAAT TAGAGGGATTTT AGTTA	T	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.|pcls:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6
2336	cg43315956	1813	GCCAAAGGGGG GACCAGAATTCC CC[C/gap]ATGCG AGCTGTTTGAGG ACTGGGAT	C	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2337	cg43315956	3757	TACAAACTTTTC CAATTTTAAAAAA [gap/A]TCAGCCA TTTCATGCAACC AGAAAC	gap	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2338	cg43315956	4535	CATGCCTGATAT TGGGATTTTTTTT [T/gap]CCAGCCT TCTTGATGCCAA GGGGCT	T	gap			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2339	cg43315956	4709	AGTTCTCATTTAA GCACTAGTGGAA [gap/T]TTTTTTTTT TTTGATATATTAG CAAG	gap	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3

2340	cg43315956	4720	AAGCACTAGTGG AATTTTTTTTTTT[gap/T]GATATATT AGCAAGTCTGTG ATGTA	gap	T			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.30E-244	3
2341	cg43935583	1599	TGTCAGCCAAAT TTGGAGGTCAAG C[G/A]TAATGTCC TTCTGATAAATAA AGCC	G	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2342	cg43935583	1605	CCAAATTTGGAG GTCAAGCGTAAT G[T/C]CCTTCTGA TAAATAAAGCCC TTGCT	T	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2343	cg43935583	1646	AGCCCTTGCTGA AGGAAAAGCAAC C[T/A]AGATCACC TTATGGATGTCG CAATA	T	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2344	cg43935583	1658	AGGAAAAGCAAC CTAGATCACCTT A[T/C]GGATGTCG CAATAATACAAA CCAGT	T	C			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2345	cg43935583	1666	CAACCTAGATCA CCTTATGGATGT C[G/A]CAATAATA CAAACCAGTGTA CCTCT	G	A			SILENT-NONCODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2346	cg43949686	415	AAACAGAAGCAG ATAAAAAAAAAA A[gap/A]GATGCA GGACTCCTTCAG TTCTTCA	gap	A			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO-REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.40E-167	

2347	cg43949686	6483	TCGATGCGTATTCTGTGGCCGCCAT[C/T]TGCGCAGGGTGGTGGTATTCTGTCA	C	T			SILENT-NONCODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO-REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.40E-167	
2348	cg43996179	140	TTTTGGTCACTGGTTTCATTTTTTT[C/T]CTTGCTCTAAACCACCTCTTCTCTG	C	T			SILENT-NONCODING	nucl_rec pt	Human Gene Homologous to SWISSPROT-ID:Q14739 LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) - HOMO SAPIENS (HUMAN), 615 aa.	1.10E-120	
2349	cg43996179	266	GTGCTGGTGGATGAGTGGGCACATG[C/gap]CCCCACCTGGGGTGGTGGAGCCGCT	C	gap			SILENT-NONCODING	nucl_rec pt	Human Gene Homologous to SWISSPROT-ID:Q14739 LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) - HOMO SAPIENS (HUMAN), 615 aa.	1.10E-120	
2350	cg43933695	3029	ATTTTCGCTTTTAACAGAGCAGCTT[C/G]CTGCTAGCGGGAGGCAGGCAATTAC	C	G			SILENT-NONCODING	nuclease	Human Gene SWISSPROT-ID:P54277 PMS1 PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTEIN PMS1) - HOMO SAPIENS (HUMAN), 932 aa.	0.00E+00	
2351	cg44128653	616	CCTGGTTCAATCGATCCTCTGGCTT[C/gap]AGTGGCTGGGACTACAGGCATTTAT	C	gap			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.|pcls:SWISSPROT-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.40E-203	19

2352	cg43944393	1834	AAGAGAGAGGG AGATAAAAGGGG GA[G/T]ACAAAAG ATGTACAGAAAT GATTTC	G	T			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2353	cg43944393	1869	GTACAGAAATGA TTTCCTGGCTGG C[C/gap]AACTGG TGGCCAGTGGG AGGTGATG	C	gap			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2354	cg43944393	1971	AGAGAGCCACCA GGAAGGCGCAT CT[T/gap]AGCAG ATGGGAGGAACT GCTGAGAG	T	gap			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2355	cg43944393	1977	CCACCAGGAAG GCGCATCTTAGC AG[A/gap]TGGGA GGAACTGCTGAG AGAAGATG	A	gap			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11

2356	cg43944393	1989	CGCATCTTAGCA GATGGGAGGAA CT[G/A]CTGAGA GAAGATGGGCA GAAAGCTG	G	A			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2357	cg43944393	297	CGAGCTTAGGAC CGCCTGCCCGG GG[C/gap]AACCC CGAACCAAGCTT TAGCCGCC	C	gap			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2358	cg43944393	317	CGGGGCAACCC CGAACCAAGCTT TA[G/gap]CCGCC GAGGCCGCGTG TCCCAAAGG	G	gap			SILENT-NONCODING	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.|pcls:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2359	cg43942083	400	GTTGAATAGGAG CCCTAACTGTAG T[T/A]ACTTCTTT CACAGCAGGGA AGGAAG	T	A			SILENT-NONCODING	nuclease	Human Gene Similar to SWISSPROT-ID:P07998 RIBONUCLEASE PANCREATIC PRECURSOR (EC 3.1.27.5) (RNASE 1) (RNASE A) (RNASE UPI-1) (RIB-1) - HOMO SAPIENS (HUMAN), 156 aa.	9.20E-83	
2360	cg43943773	113	ATTTCATATGTAA CAAAGATAAGGA [C/T]GTGTGCAG GTATAAAACAGA GGCAG	C	T			SILENT-NONCODING	nucleasei nhib	Human Gene Similar to SWISSPROT-ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19

2361	cg43943773	197	CTCATTATCCCT GAGGGGTAGGG GC[G/C]GGGGAG GAGAGGAGTCA CAGGCAGT	G	C			SILENT-NONCODING	nucleasei nhib	Human Gene Similar to SWISSPROT-ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2362	cg43943773	228	GGAGAGGAGTC ACAGGCAGTTCA CC[C/A]ACACCTG GAAAATCGATGA CTTCAT	C	A			SILENT-NONCODING	nucleasei nhib	Human Gene Similar to SWISSPROT-ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2363	cg43943773	312	GAAGTCATGAGA AGAAGGCCTTTC T[T/G]CCCAGGG ATGATGTTTCTC AGTATC	T	G			SILENT-NONCODING	nucleasei nhib	Human Gene Similar to SWISSPROT-ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2364	cg42685908	176	TACAAATATTTTT ACATTTAATAGT[C/A]ATGAAAAAG AAAAGAACTTGA AAAA	C	A			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2365	cg42685908	193	TTAATAGTCATG AAAAAGAAAAGA A[C/G]TTGAAAAA ACAACTTCAACT CTGTA	C	G			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2366	cg42685908	223	AAAAACAACTTC AACTCTGTACAA A[T/G]GTTAATAT CAAGGAGCAGCT GAAGC	T	G			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2367	cg42685908	320	TTATTAAAATATC CTTGTCTTTTTC[C/gap]ATGATATA CACATATTTTTTC TCTT	C	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2

2368	cg42685908	383	TATTATGTATTTTTAATGACAGCTT[A/C]CTTAACAACATTCATCTGGTGCTTT	A	C			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2369	cg42685908	92	AGTTATACAACTTTAAACATTGAAT[G/T]AATCATTCTTATCAAATACATCAAG	G	T			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2370	cg43947181	2974	TTCAATTGCATCATCACTGACCTGT[T/gap]AGAATTTAACCCGGAAACATCGCAA	T	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2371	cg43947181	3937	TCATGCTTTTGAACATCTTTTTTTT[T/gap]TTCATTGAAACAAATTCAAGTTCTT	T	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2372	cg43947181	3938	CATGCTTTTGAACATCTTTTTTTTT[T/gap]TCATTGAAACAAATTCAAGTTCTTG	T	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2373	cg43947181	3939	ATGCTTTTGAACATCTTTTTTTTTT[T/gap]CATTGAAACAAATTCAAGTTCTTGG	T	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10

2374	cg43988571	2942	CCACGGGCACC CCCAGCCTCAG GTG[C/gap]ACTG ACCTGCTGCCTG CCCCCAGCC	C	gap			SILENT-NONCODING	oncogene	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.|pcls:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0.00E+00	10 (10q24)
2375	cg43939230	341	GTAATAGAGGTC TTTGTAGATGGG T[A/G]CTGTATCC CATGGCAGCCCT TGCTG	A	G			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q99907 LATENT TRANSFORMING GROWTH FACTOR-BETA-BINDING PROTEIN-2 - HOMO SAPIENS (HUMAN), 1821 aa.	0.00E+00	14 (14q24)
2376	cg42716300	189	CTGCGGGAAGG TGCGGGGAGCG GAG[G/C]CATGG CCTCCGGTGCGT ATAACCCG	G	C			SILENT-NONCODING	oncogene	Human Gene SWISSPROT-ID:Q04864 C REL PROTO-ONCOGENE PROTEIN (C-REL PROTEIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	2 (2p13)
2377	cg43298442	232	TTTTTTTTTCCA CACAGCAGATGT [A/gap]TCCAAAC ACATAAAAATCT CTACAG	A	gap			SILENT-NONCODING	oncogene	Human Gene SWISSNEW-ID:Q99583 MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT) - HOMO SAPIENS (HUMAN), 582 aa.	0.00E+00	
2378	cg44008321	156	GTTGCTGATATT TATTCAAACGTC A[T/C]CCATACAA TAAAGAACTCTG CTTTT	T	C			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q63406 OST ONCOGENE - RATTUS NORVEGICUS (RAT), 872 aa.	0.00E+00	

2379	cg44008321	279	GGGGAGGGTCA CACAAGGGCGC GCA[G/gap]CTGT GCGACGAGACG GAGGCACCGC	G	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q63406 OST ONCOGENE - RATTUS NORVEGICUS (RAT), 872 aa.	0.00E+00	
2380	cg43957159	507	AGCTAGTAAACA GACAAGCCTGTC G[G/A]ACTTTGAA ACCAACTTGACC GGGTC	G	A			SILENT-NONCODING	oncogene	Human Gene TREMBLNEW-ID:G2736087 ERYTHROBLASTOSIS VIRUS ONCOGENE HOMOLOG 2 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	2.30E-260	21 (21q22.3)
2381	cg43997978	111	TTCCAGGTTTTT AATTTTCCCTGA A[T/gap]TTTTTTT TTAAACAACAAA ATTGGC	T	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2382	cg43997978	120	TTAATTTTCCCTG AATTTTTTTTTT[g ap/T]AAACAACAA AATTGGCAAGAA GAAA	gap	T			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2383	cg43997978	716	ATTTAAAGGGCA GTAGGGTGCTGT G[G/gap]CTGCAG CCTCTCCTCCAA GACGGAT	G	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2384	cg43997978	764	GATGTTGCAGGG GAGGGCCGTTA GG[G/gap]CAAGA ACCCAGCAGCTG CGTGGATG	G	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2385	cg43997978	822	ATATACCCCAGT AGTGTTCAAGGA C[A/gap]AGGCCC TCTGATCCCTAT GGCTTGG	A	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1

2386	cg43917532	511	CCTCCCCACCTTCCCCACCCTCCCC[gap/C]ACCCTCCCCATAAGCGCCCCTCCCG	gap	C			SILENT-NONCODING	oncogene	Human Gene SWISSNEW-ID:P01106 MYC PROTO-ONCOGENE PROTEIN (C-MYC) - HOMO SAPIENS (HUMAN), 439 aa.|pdb:SWISSPROT-ID:P01106 MYC PROTO-ONCOGENE PROTEIN (C-MYC) - HOMO SAPIENS (HUMAN), 439 aa.	4.20E-236	8 (8q24.12)
2387	cg43988569	383	CTGCTGGAAGAGGAAATCCCGGGGG[G/gap]CCGCCGGGCCCTCTTCGACAGCTAC	G	gap			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q13249 ABL BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 390 aa.	5.00E-213	2
2388	cg43959113	84	ACCAAGGGGAGAGGGGACGGCCCAT[T/C]GCCAATCTGTCCCAGCCCCCCGGGG	T	C			SILENT-NONCODING	oncogene	Human Gene SWISSPROT-ID:P53539 FOSB PROTEIN (G0/G1 SWITCH REGULATORY PROTEIN 3) - HOMO SAPIENS (HUMAN), 338 aa.	6.00E-182	19
2389	cg44008545	1334	TAACACTTTAAAACCAGTTACCCAA[A/T]ATCTGATTAGAAGTATAAGGTGCTC	A	T			SILENT-NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92905 JUN ACTIVATION DOMAIN BINDING PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	4.30E-179	
2390	cg43298230	1927	AACCCGTCCTCTCCCGAGTTTTTC A[T/G]AACTGAGCCCACTCGCAAGTTGGAG	T	G			SILENT-NONCODING	oncogene	Human Gene SWISSPROT-ID:P54843 TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF) - MUS MUSCULUS (MOUSE), 370 aa.	1.60E-158	
2391	cg44010709	1277	AATGCAGAGCCCCTCAGGATGGGGT[gap/G]CCCCGTCAGGGGCTGGACGGTCGTG	gap	G			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2392	cg44010709	163	CCGGGTCGTCCTCCTGCAAGGTTGCC[C/gap]CGGTGGGTCTGACGCCCAGCTGGCG	C	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)

2393	cg44010709	164	CGGGTCGTCCTC TGCAAGGTTGCC C[C/gap]GGTGGG TCTGACGCCCAG CTGGCGT	C	gap			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2394	cg44010709	191	GTGGGTCTGAC GCCCAGCTGGC GTC[C/gap]GGGA GCCGGGGTGGA GTCCTGGAGG	C	gap			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2395	cg44010709	224	GGGTGGAGTCC TGGAGGGAGGC GAA[gap/G]CGGG ATGTGGAGGGG GCCTGGAGTG	gap	G			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2396	cg44010709	267	CTGGAGTGGGG GGAGGGGCGGG TGA[G/C]GCGAG GCCCGGCCCGC CACAGTCCT	G	C			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2397	cg44010709	273	TGGGGGGAGGG GCGGGTGAGGC GAG[G/gap]CCCG GCCCGCCACAG TCCTGCCTCT	G	gap			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2398	cg44010709	68	AACTTTACTTGTT TTTTGGGAGGAG [A/G]TTAATGGGT GGGAGGGGTGA GAGGG	A	G			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)

2399	cg43918770	5017	GCGGACCACTG ACCGCTCCCCAG CG[G/gap]CAGAA GGCCTGGTCCC CTGTGGTTC	G	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.60E-140	5
2400	cg43918770	8967	TACTTTAAAGGA GTGAGCCAGAA GG[C/gap]CAAGG AGTTCGTGTGCT TCCTCCTG	C	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
2401	cg43966629	1072	ATCCTAGTTTCC CTAACTGCCTCC T[C/A]CACAGGG AGGAGTGTTGG GATCCCC	C	A			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2402	cg43966629	1089	TGCCTCCTCCAC AGGGAGGAGTG TT[G/gap]GGATC CCCCCTACCCTG TGCCCCGG	G	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2403	cg43966629	17	TTTTTTTTTTTT GAA[T/G]GATATT TAACTTTTCTTAA AAAAA	T	G			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2404	cg43966629	199	CAGTGTGTATAT TCTATTCATCAG G[G/A]AGAGTTG GGTGAGGACGT GGTGATG	G	A			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2405	cg43966629	25	TTTTTTTTTTTT GAATGATATTT[A/G]ACTTTTCTTAA AAAAAAAATCTTA A	A	G			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1

2406	cg43964295	980	AAACATCTGACG TCGTACAAAAAA A[A/gap]TTCCATC AGTATTCTGGGC ACAGAA	A	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2407	cg43964295	1351	AACAACAAAAAT ACAATTAAAAAA A[A/gap]TAAATAA TAAAGTCATTTG TGATCG	A	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2408	cg43964295	1614	GCTGCAAGGGG ACACACAACCAG GG[G/gap]TACTG TTGACTAGCTTT TTGCATAG	G	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2409	cg43964295	1960	GCTTCTCTTCTC TGTCTACCAGCG T[G/A]TACGCCG GCTGCTTGGCAA ACCGGG	G	A			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2410	cg43964295	2071	TAGACATTTTGG AGTTCTTGTTCT C[G/A]TAATCCTT GATGGGGACCG TGTTGG	G	A			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2411	cg43964295	623	GAATACTCCCTA AATGCAGTAGAT T[A/gap]AAAAAAA AAATCAAATCTA CAAGTG	A	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20

2412	cg43964295	633	TAAATGCAGTAG ATTAAAAAAAAA [A/gap]TCAAATCT ACAAGTGGTTCA GTATT	A	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20	
2413	cg43964295	633	AAATGCAGTAGA TTAAAAAAAAAA [gap/A]TCAAATCT ACAAGTGGTTCA GTATT	gap	A			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20	
2414	cg43964295	73	ATTCACACTTGC TGTTGAATAACA A[G/C]GGAATCAA GGCTCCCCTAGA TGGGG	G	C			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20	
2415	cg43964295	697	GAAAAGAAATCA GAATTTACAAAG T[A/C]AGATTGGT GTGCTTCCAAGT TCACA	A	C			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20	
2416	cg43317357	87	TGGGTCGACAG CTGGGAGGGCA GGA[T/C]TGGGG GGAAGCTGCTG GGCGCAGCC	T	C			SILENT-NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P98083 SHC TRANSFORMING PROTEIN - MUS MUSCULUS (MOUSE), 578 aa.	1.30E-106		
2417	cg43297056	228	CGCTTTGTTTTTT TTTTTTTTTTC[T /A]AAGAGAGAGG CAATTTTATTCTT CC	T	A			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103	20 (20q13.1)	
2418	cg43297056	268	TTTATTCTTCCAA AAAAATGCACCA[A/gap]GAGAGGG TGAGCACAGGA GCACCCC	A	gap			SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103	20 (20q13.1)	

2419	cg43297056	482	AACAGGGCAGC ACATGGCCCTGT TG[C/gap]CTCCA CCTGAGAGTCTG GGGAGGGG	C	gap		SILENT-NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103	20 (20q13.1)
2420	cg44129020	155	CTGCATAGGTCC AGGCCCCGGGT GG[C/gap]CCCCC AAAGGCTCCCCT CCTTCCCA	C	gap		SILENT-NONCODING	oncogene	Human Gene Similar to SWISSNEW-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.|pcls:SWISSPROT-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.	1.60E-99	
2421	cg44129020	519	GCCGGCGTGGG CGGCGGCGGCT GCG[T/C]GGTGG TGGCGGGCGTC ACTGCCGGG	T	C		SILENT-NONCODING	oncogene	Human Gene Similar to SWISSNEW-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.	1.60E-99	

2422	cg43922882	91	TGCTACCAAGGC AGTAATATTTTTC [C/T]ATATGAACC AGACCAAATACC CTTT	C	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	6.40E-91	
2423	cg43922882	94	TACCAAGGCAGT AATATTTTTCCAT [A/T]TGAACCAGA CCAAATACCCTT TAAT	A	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	6.40E-91	
2424	cg43292762	1409	CAGGCGTCACCA TCCACCTTCCCT T[gap/T]CTACAA GGACTCCATTGG ATCTGCA	gap	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2425	cg43292762	1442	GACTCCATTGGA TCTGCAAGAACA C[T/gap]TGGACC TTTGGGTTCTTT CTGGGGG	T	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2426	cg43292762	1443	ACTCCATTGGAT CTGCAAGAACAC T[T/gap]GGACCT TTGGGTTCTTTC TGGGGGG	T	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2427	cg43292762	1490	GGGGATATTTCC TAAGGCATGTGG C[C/gap]TTTATCT CAACGGAAGCC CCCTCTT	C	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2428	cg43292762	1811	GAAATTCCATAC TTCTCTCAGATG G[G/gap]AACAGT AAAGAAAGCAGA ATCAACT	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)

2429	cg43292762	1884	TTGAAAAGACCAAGACTTTTGTCTG[A/T]TCAAGTGGTTTTACAGCTACCACCC	A	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2430	cg43292762	1885	TGAAAAGACCAAGACTTTTGTCTGA[T/A]CAAGTGGTTTTACAGCTACCACCCT	T	A			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2431	cg43292762	1916	GGTTTTACAGCTACCACCCTTAGGG[G/gap]TAATTGGTAATTACCTGGAGAAGAA	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2432	cg43967603	212	TCGACTTTTTTTTTTTTTTTTCT[G/T]CCCAGCTGGCACATTTATTGGCATT	G	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:Q99471 C-MYC BINDING PROTEIN MM-1 - HOMO SAPIENS (HUMAN), 167 aa.	4.80E-77	12
2433	cg43967603	282	ATCACCAGGAAGCCACGCCCAAAGG[G/gap]TGTCCCTCTGCCCCATTTCTGCAAA	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:Q99471 C-MYC BINDING PROTEIN MM-1 - HOMO SAPIENS (HUMAN), 167 aa.	4.80E-77	12
2434	cg43101925	378	TCCTGGGGAATTCACTTCTCTTCCT[C/T]CCTCATGGAAGATGCAAGTAAAAGG	C	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSNEW-ID:P28574 MAX PROTEIN (MYN PROTEIN) (MYC-BINDING NOVEL HLH/LZ PROTEIN) - MUS MUSCULUS (MOUSE), 160 aa.]pcls:SWISSPROT-ID:P28574 MAX PROTEIN (MYN PROTEIN) (MYC-BINDING NOVEL HLH/LZ PROTEIN) - MUS MUSCULUS (MOUSE), 160 aa.	2.00E-72	14 (14q23)

2435	cg44029157	1010	CCACCCTTACTTCCTGGCCTCTTCT[G/gap]GGCTACTGCCACTGTGTGCCTTCTG	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17082 RAS-RELATED PROTEIN R-RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.10E-66	
2436	cg44029157	1012	ACCCTTACTTCCTGGCCTCTTCTGG[G/gap]CTACTGCCACTGTGTGCCTTCTGCC	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17082 RAS-RELATED PROTEIN R-RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.10E-66	
2437	cg43975131	2054	GAAGGGAACTGAAAAGCAGTAGAAG[A/G]AACAGTCAGAGATGCCTCACTGATA	A	G			SILENT-NONCODING	oncogene	Human Gene Similar to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2438	cg43975131	2081	ACAGTCAGAGATGCCTCACTGATAG[G/A]CAGGAGGCCGAACAGGTAAACCCCA	G	A			SILENT-NONCODING	oncogene	Human Gene Similar to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2439	cg43975131	578	AGCCTGACTCCTGCTGGGCACAGCC[C/gap]ACCCTGCTGGGCACAGTGACTGGAG	C	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2440	cg43975131	589	TGCTGGGCACAGCCCACCCTGCTGG[G/gap]CACAGTGACTGGAGGTTCCAGGCTG	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)
2441	cg43975131	880	CTCCCTGAGGCTGAGACGTGAAGGT[G/gap]CCCAGTCTGGGCCGTGACTCACTCT	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64	17 (17p13.3)

2442	cg43280482	2797	TGGCATATCACC CCGCACTGTGG GG[C/gap]CAGGC ACCACTAGCCTG GCTCAAAT	C	gap			SILENT-NONCODING	oncogene	Human Gene Similar to TREMBLNEW-ID:G2952331 ARG/ABL-INTERACTING PROTEIN ARGBP2A - HOMO SAPIENS (HUMAN), 666 aa.	3.90E-62	8
2443	cg43941861	604	ACCATTTCTGAC CTGCAGTTGCAG A[A/C]TAGGTGTG ACTTGCATTTAA AATAA	A	C			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P01100 P55-C-FOS PROTO-ONCOGENE PROTEIN (G0S7 PROTEIN) - HOMO SAPIENS (HUMAN), 380 aa.	2.60E-61	14
2444	cg17903042	1163	GCCGCGCAGAG CGGCCGCGGGG GGG[G/gap]CGCT GCGCACAAACCC GGGAGAAAA	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P04628 WNT-1 PROTO-ONCOGENE PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 370 aa.	7.90E-61	
2445	cg43943100	1164	TGCAAACTCTAG GACTATTATATAA [gap/T]GTAAAAAT CTCTCTTGTGAT ACTGG	gap	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2446	cg43943100	1164	TGCAAACTCTAG GACTATTATATAA [gap/T]GTAAAAAT CTCTCTTGTGAT ACTGG	gap	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2447	cg43943100	1180	TATTATATAAGTA AAAATCTCTCTT[G/C]TGATACTGG AAAGTGATTAGA ATGT	G	C			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2448	cg43943100	1182	TTATATAAGTAAA AATCTCTCTTGT[G/C]ATACTGGAA AGTGATTAGAAT GTGC	G	C			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6

2449	cg43943100	1219	GATTAGAATGTG CAAACTGATATA G[gap/C]TAGCTT TCATCCGCCTCT TAAAGGG	gap	C			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2450	cg43943100	1278	CAGGAAAGTCCA TTTAAGATGTTG G[T/A]AGGTTTAA CAAGTTGGAAT GCTGG	T	A			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2451	cg43943100	1279	AGGAAAGTCCAT TTAAGATGTTGG T[A/T]GGTTTAAC AAAGTTGGAATG CTGGC	A	T			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2452	cg43943100	1364	CTCAGAGCTACA ATGCATTTAGTA T[A/gap]TTAAAGC AGCTGACATGAT GACTTT	A	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2453	cg43979706	1456	CCCCATGTCAGG CGGAGGCGGAA GG[C/gap]CCACC GTGCCAGAGGC TGGGCACCA	C	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	
2454	cg43979706	1814	ATTTAAGTCCCT GGGCTGCCCCC TT[G/gap]GGGTG CCCCCCGCTCC CAGGTTCCC	G	gap			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	
2455	cg43979706	893	GCCCCGGTTCTG TCAGGGTCCCTA A[G/A]GGAGGAC ACTCAGGGCCTG TGGCCA	G	A			SILENT-NONCODING	oncogene	Human Gene Similar to SWISSPROT-ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	

2456	cg43268513	633	CCTCTGCCTGTG ACCCGCCGCCC GG[C/gap]CGCTA GACTGACTTCGC GCAGCGGT	C	gap			SILENT-NONCODING	oxidase	Human Gene Similar to SWISSPROT-ID:P04628 WNT-1 PROTO-ONCOGENE PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 370 aa.	7.70E-51	2
2457	cg43307658	2271	GGGCCCAGCCC CCAACCCACAGG CA[G/C]GGAGGG GCATCCCTCCCT GCCGGCC	G	C			SILENT-NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2458	cg43307658	2337	GGATGAAAACCA CAGGGATTCCG GA[T/C]GCCAGA CCCCATTTTATA CTTCACT	T	C			SILENT-NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2459	cg43307658	2472	GCTGAATAAAAC AAGGTTTTTCTA C[A/T]AAGTGGCT CTGCATGCGGC CTGCTG	A	T			SILENT-NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2460	cg43307658	2474	TGAATAAAACAA GGTTTTTCTACA A[A/T]GTGGCTCT GCATGCGGCCT GCTGGC	A	T			SILENT-NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2461	cg43096761	208	AATAGGCATACA TAAGCAATTATG T[G/A]TTTATATT CTACTCCTTTCT GAAAC	G	A			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:Q16853 COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (SERUM AMINE OXIDASE) (SAO) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	17

2462	cg43096761	24	TTTTTTTTTTTTT TTTTTTTTTT[G/T] TTTGGGCCCATT TATTGTTTATTTT	G	T			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:Q16853 COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (SERUM AMINE OXIDASE) (SAO) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	17
2463	cg44028217	36	TTTTTTTTTTTTT TGAGGCTCTGAG [G/A]GTTTATTGT CTGCCCCAGTGA GGCT	G	A			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
2464	cg44024803	166	AACATAGTTCTG ATTTTGAAGTGT T[gap/G]AGTGGA ACTCAAACAGAA ATGATTA	gap	G			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:P31513 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 3 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 3) (FMO 3) (DIMETHYLANILINE OXIDASE 3) (FMO II) - HOMO SAPIENS (HUMAN), 531 aa.	4.60E-294	1 (1q23)
2465	cg43271573	1938	TAATGCTAGAGA ATGATAACTAAG A[C/T]TTCTGTGC ATTTGAAGGTTG TTGGA	C	T			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:Q01740 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) - HOMO SAPIENS (HUMAN), 531 aa.	5.30E-293	1 (1q23)
2466	cg42849556	2051	CCACAATAAAAA AAAACCTATCAT C[gap/A]TTACAAA AACAAGACACCC AAGTCC	gap	A			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67-PHOX) - HOMO SAPIENS (HUMAN), 526 aa.	2.80E-287	1 (1q25)

2467	cg43949982	294	TTTTAATGACAATGGAAATTTGATA[T/C]ACAAAAATGGAAGGGTAAATAGAAA	T	C			SILENT-NONCODING	oxidase	Human Gene SWISSPROT-ID:Q15800 C4 METHYL STEROL OXIDASE (EC 1.-.-.-) - HOMO SAPIENS (HUMAN), 293 aa.	1.90E-169	4
2468	cg43269428	511	CGCATCAGGTAGACATGATCATCTG[C/A]ATTTCTTTTCCACGCTGCAAATCAC	C	A			SILENT-NONCODING	oxidase	Human Gene Homologous to SWISSPROT-ID:Q63448 PRISTANOYL-COA OXIDASE (EC 1.3.3.-) - RATTUS NORVEGICUS (RAT), 700 aa.	1.20E-105	
2469	cg43972840	1584	AGCCCCAGCTTATCTCCTCCTCCGC[G/gap]CTGTGTAAATGCTCCAGCACTCAAT	G	gap			SILENT-NONCODING	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.60E-168	16 (16p13.3)
2470	cg44010395	387	TGAGGATGCTGAAGGGCAGGGCTGA[T/C]CCCTTCGCCCCCTCTGAAGTTTAGG	T	C			SILENT-NONCODING	oxygenase	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.|pcls:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.20E-151	22 (22q12)
2471	cg43916857	5785	AAAAGAAGATTTTCTTTAGCAAGAA[A/T]AAAGAGGTCATGTCATTTGTTAATA	A	T			SILENT-NONCODING	peptidase	Human Gene Similar to SPTREMBL-ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17
2472	cg43916857	5788	AGAAGATTTTCTTTAGCAAGAAAA[A/T]GAGGTCATGTCATTTGTTAATAAGT	A	T			SILENT-NONCODING	peptidase	Human Gene Similar to SPTREMBL-ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17
2473	cg43916857	6366	GGAAAACAAGACTTTCCCAGCTTGT[G/A]TTACCTAGAAGCGTGAATGTATAGG	G	A			SILENT-NONCODING	peptidase	Human Gene Similar to SPTREMBL-ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17

2474	cg43948682	359	CAATTAAAAAAT CATAAAAGACTG A[G/A]TGTTTGCA ATAAAATATCAAA GAGG	G	A			SILENT-NONCODING	peptidase	Human Gene Similar to TREMBLNEW-ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	5.00E-75	10
2475	cg43254736	278	GAGCCAGGAGC CCGGGATGCGG AGA[T/C]GGGCC TCGGTCTCCACA TCCTGGCG	T	C			SILENT-NONCODING	peptidase	Human Gene Similar to SPTREMBL-ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.10E-67	
2476	cg42923012	237	AATTTGTGTGTC CTTAGGCAAAGC C[C/gap]ACCCCC TGTCTGAAGCTC AGTTTTC	C	gap			SILENT-NONCODING	peptidase	Human Gene Similar to TREMBLNEW-ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	1.00E-65	X
2477	cg41626506	291	GGAAAACAGTCG TCCTGCTGATTT C[G/C]GATTTGCC TGTGTTTGGAAA AGAGT	G	C			SILENT-NONCODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
2478	cg41626506	3179	AGCACAGCGAG CGCTCTCATTCT GA[C/gap]CTTTTT TCCTCTTCTCAG CCAACTG	C	gap			SILENT-NONCODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
2479	cg41626506	3180	GCACAGCGAGC GCTCTCATTCTG AC[C/gap]TTTTTT CCTCTTCTCAGC CAACTGC	C	gap			SILENT-NONCODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
2480	cg44913844	216	CGAGCCGAGGC CTCCTGCAGTGT TC[C/T]GCACAGC AAACCGCACGCT ATGGCT	C	T			SILENT-NONCODING	peroxidase	Human Gene SWISSPROT-ID:P04040 CATALASE (EC 1.11.1.6) - HOMO SAPIENS (HUMAN), 527 aa.	2.70E-296	11 (11p13)

2481	cg42691989	331	CTAAGGCTCCTC AGGACTGGATG GA[G/T]TAGGAG ATCTGTGTGTTG AGCAGTT	G	T		SILENT-NONCODING	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE-RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (14q24.1)
2482	cg42691989	332	TAAGGCTCCTCA GGACTGGATGG AG[T/G]AGGAGA TCTGTGTGTTGA GCAGTTC	T	G		SILENT-NONCODING	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE-RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (14q24.1)
2483	cg43951241	365	CTCAGGGGAGG CCCGCCCACAA GGG[C/gap]TTCG GGCCCCTCCTTC ATAGAGACA	C	gap		SILENT-NONCODING	peroxidase	Human Gene Similar to SWISSPROT-ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2484	cg43951241	372	GAGGCCCGCCC ACAAGGGCTTCG GG[C/gap]CCCTC CTTCATAGAGAC ACCACCCC	C	gap		SILENT-NONCODING	peroxidase	Human Gene Similar to SWISSPROT-ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2485	cg43951241	375	GCCCGCCCACA AGGGCTTCGGG CCC[C/gap]TCCT TCATAGAGACAC CACCCCTGA	C	gap		SILENT-NONCODING	peroxidase	Human Gene Similar to SWISSPROT-ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2486	cg43951241	519	AGGAAGAAGGA GGCTGGTGGTG TGT[A/T]GTGTGG GCATGTGGGAG ATGCTGGC	A	T		SILENT-NONCODING	peroxidase	Human Gene Similar to SWISSPROT-ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	

2487	cg43951241	886	GGCCCTTGCATG ATGGGCAGGGG GT[gap/A]GGGGT AGGGTGGGGTG GGCATCAGT	gap	A			SILENT-NONCODING	peroxidase	Human Gene Similar to SWISSPROT-ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2488	cg43917453	13	TTTTTTTTTTTT[G /T]TGAAATCAGA AGTTTAATATGA CAC	G	T			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2489	cg43917453	1467	ATGAACCGATTC CCCTCCACCCGT A[A/T]CTGGATTT TTCCACAAATCT CTCTT	A	T			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2490	cg43917453	164	ATTTCGATTAATT AAATTCCAGATA[G/A]AGAGAAGTA ATTTTGGAAAAG AAAT	G	A			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2491	cg43917453	1642	TCCTGACAACAT CCGTGGGGTGG GG[G/gap]CTCCC CTGAGGCCCCCT GAGGCTGCC	G	gap			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2492	cg43917453	1662	TGGGGGCTCCC CTGAGGCCCCT GAG[G/gap]CTGC CGCTCACTGGG GAAGGGCCTT	G	gap			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2493	cg43917453	270	ATTTTGGCATCA TTCTGTCCGCTC A[G/T]TAGGCCGT GTTCCCTCTGGT AGGGC	G	T			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7

2494	cg43917453	656	CGCAGTGCGTG CAGGTCGCCCT GAT[C/T]TCCTCT CCCGGGAGGGA AATGCTCG	C	T			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2495	cg43917453	661	TGCGTGCAGGTC GCCCTGATCTCC T[C/gap]TCCCGG GAGGGAAATGCT CGCAGCC	C	gap			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2496	cg43917453	90	CCGGAGGTTTCT CTTCAAACATAA G[G/T]AGTTAGAA ATTACAAGTAGG CATAT	G	T			SILENT-NONCODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2497	cg43920534	1087	CTTGGTTTTGCG CTTTTTTTTCCTT [gap/A]AAAAAAAA AAGGCCACTGAA ATGTA	gap	A			SILENT-NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
2498	cg43920534	1097	CGCTTTTTTTTCC TTAAAAAAAAAA[gap/A]GGCCACT GAAATGTATAAA ATGGTC	gap	A			SILENT-NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
2499	cg43956187	3119	CTATCAAAATAC ATGTATGTTTCA G[G/gap]ATATTT GACCTGTCATTA AAAAAAA	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q05209 PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1) - HOMO SAPIENS (HUMAN), 780 aa.	0.00E+00	7 (7q11.23)
2500	cg43930478	41	GGCCATTTGAGG GGAGCCCATGG GG[G/C]CAGGAA GGCGGCTGTGA GGCGCCCC	G	C			SILENT-NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q15171 PROTEIN PHOSPHATASE 2A 74 KDA REGULATORY SUBUNIT (DELTA OR B HOMO SAPIENS (HUMAN), 570 aa.	1.10E-306	6

2501	cg43928335	1725	GCTTAAATAATG ATTTAACAAGGA A[G/T]ACGAGTAA AAAACAATCCCA TTTCA	G	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.20E-302	11 (11q22)
2502	cg43088901	2091	CCCTCCATCCCC CTTTACCCTCTTT [G/C]CTGCAGAG AAACTTAAGCAA AGGGG	G	C			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.|pcls:SWISSPROT-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2503	cg43088901	2345	AGCCGGGGCCT TATCGGGCTCCA GC[C/gap]ATCTC ATGAGGGGAGA GGAGACGGA	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.|pcls:SWISSPROT-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2504	cg43088901	2387	GGAGACGGAGG GGAGTAGAGAA GTT[T/gap]ACAC AGAAATGCTGCT GGCCAAATA	T	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.|pcls:SWISSPROT-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2505	cg43302847	2299	ATGCTCATGTCC CTGTCCCCAGGC C[C/gap]AGCCCT CCTTCAGGGGA GTTGAGGT	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE-NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)

2506	cg43302847	2419	CTGGGTGGCCATCCTACCCAGCGTG[gap/G]CCCAGGCCGGGAAGAGCCACCTGGC	gap	G			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE-NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
2507	cg43302847	2516	AAGCGACTCTCCTGTTTGGAACGGC[gap/A]AAAAAAAAATTTTTTTTTCTCTTTT	gap	A			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE-NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
2508	cg44012067	105	TTTTAATTTTTTTTTTTTTTTTTT[C/T]TCAACTTGCTCAGTGCTTTATTGAA	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P30305 M PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 566 aa.	1.00E-285	20
2509	cg43984117	145	TATAGGAGGGGAGGCGCAGGCGGGG[C/gap]CCCCCTGCTGACCCTCTCTCTGGGG	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2510	cg43984117	188	CTCTGGGGGTCTTCCTATGGCGGGG[C/gap]CCTATTGCTTGAGTGGGGGAGGAGC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2511	cg43984117	190	CTGGGGGTCTTCCTATGGCGGGGCC[C/gap]TATTGCTTGAGTGGGGGAGGAGCCA	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	

2512	cg43984117	295	CTCCCCACAGAA TGCCCAGGCTGT G[C/gap]CCCCAG CCCCAGCTGCTC CACCTCC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2513	cg43984117	299	CCACAGAATGCC CAGGCTGTGCC CC[C/gap]AGCCC CAGCTGCTCCAC CTCCTTCC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2514	cg43984117	324	CAGCCCCAGCT GCTCCACCTCCT TC[C/T]TCTCTGT CCAGGGAGCAG ACCCTCT	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2515	cg43984117	95	TAAAATAGCTGG GGAGGGGGGTG AG[C/gap]CCCAG CCTAGCCCCACC ATGGGGCT	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2516	cg43984117	98	AATAGCTGGGGA GGGGGGTGAGC CC[C/gap]AGCCT AGCCCCACCATG GGGCTATA	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2517	cg43139469	1922	CTCAAGCCTGGA GTCTGAGGCTTG C[C/gap]TACAAG AGGAGAGAAAGT AGATAGG	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7.00E-259	5 (5q31)

1437	cg44922718	1447	CAAATGATGAAGAATGGGCCATGGC[C/gap]AGCATGCAGCATTATTTCCATTGTC	C	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1438	cg43931745	278	GCCTGGGCAGTAGGGAGAACTACCC[C/G]CTATCTCTCCAGGTACATCCCAGCT	C	G			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q02395 M96=METAL RESPONSE ELEMENT DNA-BINDING PROTEIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 373 aa.	2.00E-80	6
1439	cg43931745	369	GTGTGAATGGGGAGCTGGGCAGAGG[C/gap]AGGCTGTTCAGAAGATGCCCCCTCC	C	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q02395 M96=METAL RESPONSE ELEMENT DNA-BINDING PROTEIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 373 aa.	2.00E-80	6
1440	cg43920750	1030	CTGCCGCGACCCGGACTGCGCGCCA[G/gap]CACCCCCCTGCCGACAGCTCCGTCA	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.70E-77	4
1441	cg43918693	1192	GGGGACGAGTTGATAAGCTGGGCGG[G/T]GGGGGGGGGGTCCACTGTCACTTGA	G	T			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6
1442	cg43918693	2361	GATTTTTTTCTATACAGGGAGGTTT[A/gap]AAAAAAAATACTTGAACAGTTTGCC	A	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6
1443	cg43918693	2443	TTCTCATATTTTTTTAGGTGTAAAA[T/A]AAAGATTCAGTAATTTTAACTCAGA	T	A			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6

1444	cg43920744	180	GACAACACAACTTAAAAATGAACTT[A/C]CTTCCATTCCCTAAAGTTGCATGTT	A	C			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1445	cg43920744	196	AATGAACTTACTTCCATTCCCTAAA[G/A]TTGCATGTTGAATGAACAGAATCCC	G	A			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1446	cg43920744	365	GCAGGCACCAAATTAAAAAAAAAAA[gap/A]GGGAGGGCTCATGAGCATAAGAAAC	gap	A			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1447	cg43920744	365	GCAGGCACCAAATTAAAAAAAAAAA[gap/A]GGGAGGGCTCATGAGCATAAGAAAC	gap	A			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1448	cg43920744	58	TTTTTGTTTAAAAAGGCTTTATTCA[T/gap]TTTTTGATCAGGGAAAAGGACAATC	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1449	cg43920744	63	TTTAAAAAGGCTTTATTCATTTTTT[gap/T]GATCAGGGAAAAGGACAATCTCAAT	gap	T			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1450	cg43144895	903	TGAGCCCACTGTGGTGCTCCTGCAG[G/gap]CTGAGCCACAACTGCTGGACACACA	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.40E-59	11

1451	cg43327954	984	AACTGAAGCAGGCCTTGAAGCCTTG[T/C]CCCCTTGAGGACAAGAAACCCGAGG	T	C			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
1452	cg43327954	985	ACTGAAGCAGGCCTTGAAGCCTTG[T/C]CCCTTGAGGACAAGAAACCCGAGGA	C	T			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
1453	cg43936210	235	TAAATCAGTGGTGGAAGAGCCGAA[G/gap]GTTCGTATGAGCGAGGATGATTCCC	G	gap			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1454	cg43936210	236	AAAATCAGTGGTGGAAGAGCCGAAG[G/gap]TTCGTATGAGCGAGGATGATTCCCA	G	gap			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1455	cg43936210	308	CAACTTTGTCAGCAGCAGAACCGGA[G/gap]GAGCCGCAATGTACGCCACACCAC	G	gap			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1456	cg43936210	587	ACTTCATCGAAAGCACTTGTGGATG[G/gap]TGTCTAAGCCACCAATAGTTTGCCT	G	gap			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1457	cg43946971	245	AGCAGTTTGCCATGGAGAGCTTGGG[G/C]CTGCACACGGTGACCCTTAGTGATG	G	C			SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52	6 (6p21.3)

1458	cg43917203	916	TCATCTTAGAAA GGTCTGGTCGCA T[C/gap]CTACGG GCCCGCTTCTTG CTGCTCT	C	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to SWISSPROT-ID:O14646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1) - HOMO SAPIENS (HUMAN), 1709 aa.	5.90E-50	14
1459	cg43980504	81	CACAGAACTATT GTAAAACAATAT T[T/C]TCAGTCGG TGATCATTGTAA TATAC	T	C			SILENT-NONCODING	dna_rna_bind_inhib	Human Gene Similar to SWISSNEW-ID:P41134 DNA-BINDING PROTEIN INHIBITOR ID-1 (ID) - HOMO SAPIENS (HUMAN), 154 aa.|pcls:SWISSPROT-ID:P41134 DNA-BINDING PROTEIN INHIBITOR ID-1 (ID) - HOMO SAPIENS (HUMAN), 154 aa.	6.60E-74	20 (20q11)
1460	cg43299462	639	AACTGCAGAAAG GGCATTTAAAAG T[C/T]TTTTTCATA AATAACGAATAT CACA	C	T			SILENT-NONCODING	dna_rna_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.|pcls:SWISSPROT-ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.20E-67	3 (2p25)
1461	cg43299462	726	TTAGTTTTCCTTC CATTTTTTTTTT[g ap/T]CTTTTTAAA AAGGTCCATTCA ACTT	gap	T			SILENT-NONCODING	dna_rna_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.|pcls:SWISSPROT-ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.20E-67	3 (2p25)
1462	cg43971258	1074	AGAGAAAGAAAA CCAAAAGAAGTC C[C/gap]GCTACA GTGACCTGCAAC GCGCGCA	C	gap			SILENT-NONCODING	dna_rna_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.|pcls:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)

1463	cg43971258	146	TAAAGAACAATA CTTTTTTTTTTTT[A/T]CACAAGTGT TTAAAAATCGTTT ATT	A	T		SILENT-NONCODING	dna_ma_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.|pcls:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1464	cg43971258	245	CAGAAAGTCACC TTCCTGTAAAAA A[gap/A]GGTACA AAACCTATATAC TCTATTA	gap	A		SILENT-NONCODING	dna_ma_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.|pcls:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1465	cg43971258	343	AAGACCAGCTCT GCCGCCGCCTT GG[C/gap]ATAGT TTGGAGAGCAGC CACTCCTT	C	gap		SILENT-NONCODING	dna_ma_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.|pcls:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)

1466	cg43971258	389	TCCTTCCACACC TCCACGCTCTGA A[A/G]AGACCTTA GAACTTGGGGGT GGGGT	A	G			SILENT-NONCODING	dna_rna_bind_inhib	Human Gene Similar to SWISSNEW-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.|pcls:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1467	cg43949306	169	CTTCTCTATTTAC AATCTGAAGAAT[T/C]TCTCCTTTG GAAAACTTCAAT CCTG	T	C			SILENT-NONCODING	dynein	Human Gene SWISSPROT-ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	0.00E+00	14
1468	cg43947402	256	CTTTTGAAGGAA AAGGCAGAGGC AT[G/T]TTTACAT TATCCCAGAAAA CAGAAT	G	T			SILENT-NONCODING	dynein	Human Gene SWISSPROT-ID:Q90828 DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A) - GALLUS GALLUS (CHICKEN), 515 aa.	3.70E-214	3
1469	cg43972836	644	GGAGCTGCTGA GTTCTGGACACA GC[G/A]TTTCTTT CCCAGAATGAGA CTGGCT	G	A			SILENT-NONCODING	dynein	Human Gene Homologous to SPTREMBL-ID:Q12019 SIMILARITY NEAR N-TERMINUS TO S. CEREVISIAE DYNEIN HEAVY CHAIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 4910 aa.	1.20E-132	6
1470	cg43932150	76	ACCGCCTTCTCA TCGCTCCTGGAA G[G/gap]TCCCGA GCGCGACACCAT GTCGGAG	G	gap			SILENT-NONCODING	dynein	Human Gene Similar to SWISSPROT-ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	1.10E-89	

1471	cg43923118	1830	GCTGCTCCATGG TGAAAACCGACA G[G/gap]CCGCCG AGGCACGCTCC GGGCTCCG	G	gap			SILENT-NONCODING	elastasei nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1472	cg43923118	1840	GGTGAAAACCGA CAGGCCGCCGA GG[C/gap]ACGCT CCGGGCTCCGA GCTGGGGGC	C	gap			SILENT-NONCODING	elastasei nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1473	cg43923118	1863	GGCACGCTCCG GGCTCCGAGCT GGG[G/T]GCGAG GTCAGGAAGGA GGA	G	T			SILENT-NONCODING	elastasei nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1474	cg42184167	207	CAGGTGCAGCAA GGACCGGCTCC CT[C/gap]TCACT GGGGAACGAAA CAGGCCATC	C	gap			SILENT-NONCODING	elastasei nhib	Human Gene Similar to SWISSPROT-ID:P19957 ELAFIN PRECURSOR (ELASTASE-SPECIFIC INHIBITOR) (ESI) (SKIN-DERIVED ANTILEUKOPROTEINASE) (SKALP) - HOMO SAPIENS (HUMAN), 117 aa.	1.60E-60	20
1475	cg43958656	2602	TTTTTTGGTGAA GTACTGAACTTG C[gap/C]TTTTTTT CCGGTTTCTACA TGCAGA	gap	C			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
1476	cg43958656	521	CGTTTCCAGCCC CCAATCTCAGAG C[G/C]GAGCCGA CAGAGAGCAGG GAACCGG	G	C			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6

1477	cg43958656	546	GGAGCCGACAG AGAGCAGGGAA CCG[G/gap]CATG GCCAAAGCCGC GGCGATCGGC	G	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
1478	cg44017749	14845	CGTTTTAATAATT TTTGCTGAATTC[C/gap]TTTACAAC TAAATAACACAG ATATT	C	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0.00E+00	12
1479	cg43982507	3293	ACAAATAATACC CCCGTCGGAATG G[T/gap]AACCGA GCCAGCAGCTG AAGTCTCT	T	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
1480	cg43982507	533	CCTCCCAGCCCC CACCTTCTTCCT C[C/gap]TTTCGG AAGGGCTGGTAA CTTGTCG	C	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
1481	cg43982507	594	CGGCGGCGGCG GCGGCGGCGGC GGC[gap/G]ACCA TCCAGGCGGGC ACCATGGGCA	gap	G			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
1482	cg43982507	594	CGGCGGCGGCG GCGGCGGCGGC GGC[gap/G]ACCA TCCAGGCGGGC ACCATGGGCA	gap	G			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)

1483	cg43965833	3513	GTTTGGTTGCTG GGGGGGCTTTTT T[A/G]GGTTTTGG GGCATTTGTTTT TTGTA	A	G		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00
1484	cg43965833	3763	GTTTATATGTGT ATGTGTGTGACA G[A/G]AAAATCTG TAGAGAAGAGGC ACATC	A	G		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00
1485	cg43965833	3890	AAAAGCCTTTGG AAATCTGGATCA G[A/G]AAATAGAT ACCATGGTTTGT GCAAT	A	G		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00
1486	cg43965833	4483	TTGGCTTAAGTC AGAACAACTGGC C[A/C]AAATTGAA GTCATATTTGAG GGGGG	A	C		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00
1487	cg43965833	4484	TGGCTTAAGTCA GAACAACTGGCC A[A/C]AATTGAAG TCATATTTGAGG GGGGA	A	C		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00
1488	cg43965833	4502	CTGGCCAAAATT GAAGTCATATTT G[A/T]GGGGGGA AATGGCATACGC AATATT	A	T		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00
1489	cg43965833	4514	GAAGTCATATTT GAGGGGGGAAA TG[G/gap]CATAC GCAATATTATATT ATATTGG	G	gap		SILENT-NONCODING	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00

1490	cg44007516	377	TAATAAAAATAAC TGGAGCAGAGAA [A/gap]GCTTTAG GAGTTATACCAT TAGTTC	A	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:Q03933 HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2) (HSTF 2) HOMO SAPIENS (HUMAN), 536 aa.	6.20E-283	
1491	cg43945212	2872	TGTCCTGTGTCT ATGTACCTCTAG C[A/gap]TGTTCTT TTTTGTACTTTTC TGGTT	A	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN AI REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.80E-232	7
1492	cg43945212	926	GTCCCCTTCCCC TCCCCTCCCGGC G[G/C]AAAGCCC CCCGAAACCAAC AAAGCT	G	C			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN AI REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.80E-232	7
1493	cg43945167	405	TGCTACCACCAC CAAGCCCTGTGT C[G/A]CGACGGC AGCGGCTGCAG TCACCAG	G	A			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)
1494	cg43945167	475	GACACCCGTGC CAGCCCCAGCC ACC[C/gap]TGAC GGCGGGCTGTC CACGGAAATG	C	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)

1495	cg43945167	561	CTTCCCTGCCGGGCTGGGCTCCCCA[A/G]TGCCTTCAGAGTTCGTTGTGCCGAG	A	G			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)
1496	cg38775224	1064	TGGTAACCACAGAATTAATAACTGT[A/gap]CTACCCTGACAAGCTATATACATGT	A	gap			SILENT-NONCODING	eph	Human Gene SWISSPROT-ID:Q13790 APOLIPOPROTEIN F PRECURSOR (APO-F) - HOMO SAPIENS (HUMAN), 308 aa.	1.30E-161	12
1497	cg43262939	524	CCTTCAATAGCATGTCAAGTGGAGT[G/A]AAAAAAGAATTTGGCCATGAATTTG	G	A			SILENT-NONCODING	eph	Human Gene Homologous to SWISSPROT-ID:P08519 APOLIPOPROTEIN(A) PRECURSOR (EC 3.4.21.-) (APO(A)) (LP(A)) - HOMO SAPIENS (HUMAN), 4548 aa.	4.60E-108	
1498	cg43918531	1635	GAATGATTTTGAAGATTGATGACAT[T/C]CGTAAGCCTGGAGAATCTGAAGAAT	T	C			SILENT-NONCODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS KODAKARAENSIS, 546 aa.|pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
1499	cg43918531	1729	TAAGTAAATGGATGTCTCGTGATGC[G/A]TCTACAGTTATTTATTGTTACATCC	G	A			SILENT-NONCODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS KODAKARAENSIS, 546 aa.|pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

1500	cg43918531	1843	CAAAGCTGTGTA ATCGTGGGGGTA C[T/C]ATCTCAAC TGCTTTTGTATTC ATTG	T	C			SILENT-NONCODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS KODAKARAENSIS, 546 aa.|pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
1501	cg43944783	39	TTTTTTTTTTTTT TTTTTTTTTTTT[A /T]TAACCACGCC CAACTGGCTTGT TTT	A	T			SILENT-NONCODING	eph	Human Gene Similar to SWISSPROT-ID:P15705 HEAT SHOCK PROTEIN STI1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 589 aa.	2.80E-74	11
1502	cg43984905	2387	CTAGGCTGGAG GAAGCCAGTGG GGT[C/gap]CCCC CTGAGTGGGCT GGGCCCTCTG	C	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1503	cg43984905	2392	TGGAGGAAGCC AGTGGGGTCCC CCC[gap/C]TGAG TGGGCTGGGCC CTCTGTCCAC	gap	C			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1504	cg43984905	2440	CACATGTGGGGA CAGGGCTGGTG TG[G/gap]CTGCT CCCAGCCTCTTG CTCAGAGC	G	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

1505	cg43984905	2575	GTCCTTCATTCC GTTAGGAATAAC A[C/A]TGCAGCC CTCTCCAACCTC CGGCCA	C	A			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1506	cg43984905	2599	ACTGCAGCCCTC TCCAACCTCCGG C[C/gap]AGCGAG TGGTCAAGGATT TTTATAA	C	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1507	cg43274299	2011	CTGCTCAGACCT GTGACCCCGGC GG[G/gap]ACCCC CATGTCCTCCGC TCCGCCCG	G	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1508	cg43274299	2149	GTCCCCCGGGG CTCCCGGTCCTC TG[gap/G]CATGT CTCAGGCTGAGC TCCCTCCC	gap	G			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1509	cg43274299	2156	GGGGCTCCCGG TCCTCTGCATGT CT[gap/T]CAGGC TGAGCTCCCTCC CCCGCGGT	gap	T			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1510	cg43274299	2170	CTCTGCATGTCT CAGGCTGAGCTC C[C/gap]TCCCCC GCGGTGCCTTC GCCCTCTG	C	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7

1511	cg43274299	2176	ATGTCTCAGGCTGAGCTCCCTCCCC[C/gap]GCGGTGCCTTCGCCCTCTGGCTGCA	C	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1512	cg43274299	2180	CTCAGGCTGAGCTCCCTCCCCCGCG[G/gap]TGCCTTCGCCCTCTGGCTGCAAATA	G	gap			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1513	cg43972012	102	CAGGGTTCCTGGCTGGGCAGCACAG[G/gap]CCTGGGGCGACACTCCTGTCTTGTC	G	gap			SILENT-NONCODING	esterase	Human Gene SPTREMBL-ID:Q16837 ACID SPHINGOMYELINASE (EC 3.1.4.12) (SPHINGOMYELIN PHOSPHODIESTERASE) (NEUTRAL SPHINGOMYELINASE) - HOMO SAPIENS (HUMAN), 629 aa.	0.00E+00	11 (11p15.4)
1514	cg44011461	172	ATTTATCAAGGTTTTCATTGCTTTT[gap/T]ATTCAATGAGGTTTGGAACATGAGA	gap	T			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1515	cg44011461	188	CATTGCTTTTATTCAATGAGGTTTG[G/C]AACATGAGAGGCCAAAAATGAGGAG	G	C			SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)

1516	cg44011461	241	CATTTTGGGGAA TCCTCTATAAAG A[A/gap]TATAAGT TAAGAAAGTTGT CCAAGA	A	gap		SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1517	cg44011461	251	AATCCTCTATAA AGAATATAAGTT A[A/gap]GAAAGT TGTCCAAGATGA AAATAAT	A	gap		SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1518	cg44011461	255	CTCTATAAAGAA TATAAGTTAAGA A[A/gap]GTTGTC CAAGATGAAAAT AATAGGA	A	gap		SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1519	cg44011461	524	TGCATTTCTCCT GGTACAGCTGGA G[C/gap]TGGTTC TCATTAACACTG AACTCTT	C	gap		SILENT-NONCODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1520	cg43984524	860	TATCACCCTGAA CGCGCCTGATCT C[A/G]TCTGATCT CGGAAGCTAAGC AGGGT	A	G		SILENT-NONCODING	esterase	Human Gene Similar to SPTREMBL-ID:P70665 SIALIC ACID-SPECIFIC 9-O-ACETYLESTERASE - MUS MUSCULUS (MOUSE), 541 aa.	3.20E-99	

1521	cg43319420	1886	CTGCAGTTCTGG ACGGGCTGGCC GA[G/gap]TGCGC GGGATCCTTGTG CAGGGAAG	G	gap		SILENT-NONCODING	esterase	Human Gene Similar to SWISSNEW-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.|pcls:SWISSPROT-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
1522	cg43319420	1916	CGGGATCCTTGT GCAGGGAAGAG CT[G/gap]CCCTG GGCACCTGGCA CCACAAGAC	G	gap		SILENT-NONCODING	esterase	Human Gene Similar to SWISSNEW-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.|pcls:SWISSPROT-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
1523	cg43934722	737	GGGATTTTGTGG ACGTCTCCGTGC A[G/T]GAACTGCT GGACTGTGGCC GCTGTG	G	T		SILENT-NONCODING	fgf	Human Gene TREMBLNEW-ID:G2738520 FGF-1 INTRACELLULAR BINDING PROTEIN - HOMO SAPIENS (HUMAN), 372 aa.|pcls:TREMBLNEW-ID:G2738522 FGF-1 INTRACELLULAR BINDING PROTEIN - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 372 aa.	9.80E-184	
1524	cg43281831	2016	TCCTTTAACCAC TGCCCTCTCCTT C[T/gap]TTCTCCT TCAAGGTTCTTT CCCCCT	T	gap		SILENT-NONCODING	fgf	Human Gene Similar to TREMBLNEW-ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	9.20E-83	4

1525	cg43281831	2017	CCTTTAACCACT GCCCTCTCCTTC T[T/gap]TCTCCTT CAAGGTTCTTTC CCCCTC	T	gap			SILENT-NONCODING	fgf	Human Gene Similar to TREMBLNEW-ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	9.20E-83	4
1526	cg43919380	1038	CGAGGGGTCCT CACCTGGTTGAC CC[C/gap]AAAAA TGTTCCCTTGAC CATTGGCT	C	gap			SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1527	cg43919380	1257	TTGCCTCTTGCA GGCTGAGTCCCT C[A/C]ATGCAAAA GTGGGGCTAAAT GAAGT	A	C			SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1528	cg43919380	2230	TGTACTAAGGAG CATGATTTTAAG A[G/T]GCTTTGGC CCAATGCCTATA AAATG	G	T			SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1529	cg43919380	2240	AGCATGATTTTA AGAGGCTTTGGC C[C/gap]AATGCC TATAAAATGCCC ATTTCGA	C	gap			SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)

1530	cg43919380	3274	TTAAGGTGCCTA CTGTGTGCTAGG C[A/gap]CTGTAC TGGATACTGGGG ACCTTGT	A	gap		SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1531	cg43919380	3702	AAGTCTCATAGC CAGCTCCTGTCA C[G/A]TGACTCTC ATATGGATTCAT TTTCG	G	A		SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1532	cg43919380	395	GGGCTACTCTGA GAAGAAGACACC A[G/A]GGGGATT CCTCTTCCCCTG GGACAG	G	A		SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1533	cg43919380	404	TGAGAAGAAGAC ACCAGGGGGATT C[C/T]TCTTCCCC TGGGACAGCACT GAGCG	C	T		SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)

1534	cg43919380	406	AGAAGAAGACAC CAGGGGGATTC CT[C/T]TTCCCCT GGGACAGCACT GAGCGAG	C	T		SILENT-NONCODING	fgf	Human Gene Similar to SWISSPROT-ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA-ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1535	cg43918792	691	ACCGCAAACAGC AAAGACTATCCC A[A/C]CTTTCTAT TAACAGTGCCAA GATTA	A	C		SILENT-NONCODING	fgf	Human Gene Similar to TREMBLNEW-ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	1.70E-56	13
1536	cg43918792	697	AACAGCAAAGAC TATCCCAACTTT C[T/G]ATTAACAG TGCCAAGATTAT AACTG	T	G		SILENT-NONCODING	fgf	Human Gene Similar to TREMBLNEW-ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	1.70E-56	13
1537	cg43937658	1026	CAAGGCAGTAA CCCCAGCGACC AG[C/gap]TGCTG CTGCTGCACGGT GAGGAGGA	C	gap		SILENT-NONCODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1538	cg43937658	353	AGCCTCAGCAG GGCCGGTCCAG ACA[T/C]GGCTGA GTCCTGTGCTGC CCTGGAG	T	C		SILENT-NONCODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1539	cg43937658	561	CCACAGAAATAC CCATGGCTGTGG G[G/gap]CTGTGA CCAGCAGTGGCT GATTAGG	G	gap		SILENT-NONCODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1540	cg43937658	898	TTTTTTTGGTGG TTTTCTTAAAAA [gap/A]GCCTTTG AGTTGCAGGTCA GGTGAG	gap	A		SILENT-NONCODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16

1541	cg43937658	950	TGGTTCTGGAAG TACCGGAAGTTC T[G/T]TTGGTATG AGAGAGACTTGT CTACA	G	T			SILENT-NONCODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1542	cg43284508	306	CTCTATCCCATA CCTTTGCAAAGG A[G/A]GGGAGGG GTCTACAAGCCA GAACTT	G	A			SILENT-NONCODING	fgfrecept or	Human Gene Similar to SPTREMBL-ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1543	cg43284508	443	ACATCAGAACCA CTGACTGGTAGA G[C/T]CCTTGGAA ATCATACAGTCC ACCCA	C	T			SILENT-NONCODING	fgfrecept or	Human Gene Similar to SPTREMBL-ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1544	cg43284508	475	AAATCATACAGT CCACCCATCCCC C[G/A]CCAGACA CATGGACACACC GAGGCT	G	A			SILENT-NONCODING	fgfrecept or	Human Gene Similar to SPTREMBL-ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1545	cg43284508	881	CCACGCCCATAT GAGGGGTGGAG AG[G/gap]AGAAG CCAGCAGCACTG GGGTGAGC	G	gap			SILENT-NONCODING	fgfrecept or	Human Gene Similar to SPTREMBL-ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1546	cg43284508	883	ACGCCCATATGA GGGGTGGAGAG GA[G/gap]AAGCC AGCAGCACTGG GGTGAGCCT	G	gap			SILENT-NONCODING	fgfrecept or	Human Gene Similar to SPTREMBL-ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1547	cg43320667	576	ATTAAAAAGGTC ACCAGCCCGCC AG[G/gap]TGCCA GAAGCCACCGG GTATCCTTG	G	gap			SILENT-NONCODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)

1548	cg43320667	674	TCTCTGCGTGGT GATGGTGTCTGG A[C/gap]TCGCCA CTCGAGGTAGGT TGAGATG	C	gap			SILENT-NONCODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
1549	cg43975899	1613	TTTTACTCACATT CTGTTGTTCAGT[gap/T]CCTCTGCA CTGGGAATTTAT TTATG	gap	T			SILENT-NONCODING	gaba	Human Gene SWISSPROT-ID:P14867 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)
1550	cg43975899	1664	TCTCAACGCAGT AATTCCCATCTG C[gap/C]TTTATTG CCTCTGTCTTAA AGAATT	gap	C			SILENT-NONCODING	gaba	Human Gene SWISSPROT-ID:P14867 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)
1551	cg43299024	3522	TTTCTCCCTAGA TCGCACTGTGGG C[C/T]GGGGCCC TGGAGGGCTGC TCTGTGT	C	T			SILENT-NONCODING	glucoamylase	Human Gene TREMBLNEW-ID:G2826521 MALTASE-GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1552	cg43299024	3529	CTAGATCGCACT GTGGGCCGGGG CC[C/gap]TGGAG GGCTGCTCTGTG TTAATAAG	C	gap			SILENT-NONCODING	glucoamylase	Human Gene TREMBLNEW-ID:G2826521 MALTASE-GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1553	cg43299024	3718	GCTGCTCTGCCC CAACGCGACCG CT[G/T]CCCGGC TGCCCAGAGGG CTGGATGC	G	T			SILENT-NONCODING	glucoamylase	Human Gene TREMBLNEW-ID:G2826521 MALTASE-GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1554	cg43299024	3744	CCCGGCTGCCC AGAGGGCTGGA TGC[C/gap]TGCC GGTCCCCGAGC AAGCCTGGGA	C	gap			SILENT-NONCODING	glucoamylase	Human Gene TREMBLNEW-ID:G2826521 MALTASE-GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

1555	cg43992911	397	CTTCTTCCAAGA TTTCACGTCTTG G[C/T]GGCCGTT CCAAGGAGCGC GAGGTCG	C	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	.	7
1556	cg43943531	2247	TAAATGTCACGT CCAGCTCTGATA T[G/gap]CTTCGC ACTGAGCACATC ACATTTA	G	gap			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	(11q23.3)	11
1557	cg43943531	2343	TGTAAGAACAAA ACTGGATGGCAT C[A/C]GAATTGTC TGGAAGTTTTGT CTTGG	A	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	(11q23.3)	11
1558	cg43943531	2372	TTGTCTGGAAGT TTTGTCTTGGGC A[G/T]TATGGGCT GGGCCAAATGAA ATGAT	G	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	(11q23.3)	11
1559	cg43943531	2373	TGTCTGGAAGTT TTGTCTTGGGCA G[T/G]ATGGGCT GGGCCAAATGAA ATGATT	T	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	(11q23.3)	11
1560	cg44021330	3335	AACACACATGAT GACTGAGGCATT C[G/A]GGAACCC CTTCATCCAAAA GAATAA	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q12860 CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) - HOMO SAPIENS (HUMAN), 1018 aa.	0.00E+00	(12q11)	12
1561	cg43997653	2551	GAGCTATTTTTA CCTCCCGCCTCC C[C/T]TGCTGGTC CCCCCACCTGAC GTCTT	C	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P50895 LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN) - HOMO SAPIENS (HUMAN), 628 aa.	0.00E+00		

1562	cg44003301	1920	TGAGATAAAAGATGTACTTGTGACC[A/G]TTGTAACAATAGCACAAATAAAGCA	A	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16671 PLATELET GLYCOPROTEIN IV (GPIV) (GPIIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) - HOMO SAPIENS (HUMAN), 471 aa.	2.00E-254	7 (7q11.2)
1563	cg43957605	150	TTATAGAAAGTTGCAGTTAAAAACG[C/T]TTTCTCCAAAATAAAAAGACAAATG	C	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)
1564	cg43957605	510	CAAATGCTGGAGAGGGGCATACAGT[G/gap]GGTTCCCCCATTCTACAAGCTTAGT	G	gap			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)
1565	cg43926590	415	TTCAGACAATTCAGCCTTTATTTTA[G/A]AAAATAATTCTGTAGCTTCCACTTT	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P26572 ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I) - HOMO SAPIENS (HUMAN), 445 aa.|pcls:SWISSPROT-ID:P26572 ALPHA 1,3-MANNOSYL-GLYCOPROTEIN BETA 1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I) - HOMO SAPIENS (HUMAN), 445 aa.	4.20E-245	5 (5q35)

1566	cg44003218	158	GATTCTTTCTGT GACTCATCAGTT C[A/C]TTTCCTGT AAAATTCATGTC TTGCT	A	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16671 PLATELET GLYCOPROTEIN IV (GPIV) (GPIIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) - HOMO SAPIENS (HUMAN), 471 aa.	2.40E-242	7 (7q11.2)
1567	cg42360692	1557	AGAAGAAGGATA CACAAAACGTAC C[C/gap]TTATCT GTTTCCCCTTCC TTGTCAG	C	gap			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPROTEIN BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1568	cg42360692	1584	TATCTGTTTCCC CTTCCTTGTCAG C[G/A]TCGGGAA GATGGTATGAAG TCCTCT	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPROTEIN BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1569	cg42360692	1826	GCCGATGCATAA AGTCAGCCTGTT C[A/C]AAGTGCTC AGGGACTTAGCA AAATG	A	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPROTEIN BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)

1570	cg42360692	1914	TAAATGTGACCA TTTTTCTGGTAT G[gap/C]AATAAA CTTACAGCAACA AATAATC	gap	C		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPROTEIN BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1571	cg42360692	1914	TAAATGTGACCA TTTTTCTGGTAT G[gap/C]AATAAA CTTACAGCAACA AATAATC	gap	C		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPROTEIN BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1572	cg43924995	1830	GGCCAAATTTTG ATCCTAACCTTG A[A/C]GTATGCCT TGAACTTATTAA CATGG	A	C		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.20E-222	X (Xq24)
1573	cg43987514	76	TTTTTTTTTTTT TTGGCAGGTAAA [A/G]GAAAAGACT TTATTAATAATCA GTG	A	G		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-215	

1574	cg43301245	232	TTCCTAAGTGAA GGTTTCAAGCTG G[G/gap]CTTTGC AGGGGGTATAAT TAGTATG	G	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3.00E-210		1
1575	cg43301245	334	ATGGTGTCCTTT GATAAGGAGGG CT[G/A]GGGGGC AGGGAGTTGAAG AAATTCC	G	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3.00E-210		1
1576	cg43301245	399	GATCTGTAAACA TTTCCATTAATCA [gap/T]ACAAGTG TGTACTAATCCC GAGTCT	gap	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3.00E-210		1
1577	cg43958670	1152	CATACGGAGTTC TCTTTGGGAAAA C[G/A]ACAAGACT ACAGTGTTCACT TCGCA	G	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)

1578	cg43958670	15	TTTTTTTTTTTTT T[T/A]TTTTTTTCC AAATGTACAATTT TAT	T	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1579	cg43958670	16	TTTTTTTTTTTTT TT[T/A]TTTTTTTCC AAATGTACAATTT TATT	T	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1580	cg43958670	174	GAATTCATATAC GCTTCTGTCATT T[A/C]AACAAACT TCCAGAGAAAAC TGGTC	A	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1581	cg43958670	1953	AATCTATTCAGC CTCTCTGCTCTG C[A/T]GGAGTGG TTGATTTAGTCT GGTAAG	A	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1582	cg43958670	3091	CTCGCGGCGGC CGGGAGGCTCC ATG[C/G]GCGGC GCGGGAAGACG CTGTTATTT	C	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1583	cg43958670	3092	TCGCGGCGGCC GGGAGGCTCCA TGC[G/C]CGGCG CGGGAAGACGC TGTTATTTC	G	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)

1584	cg43958670	3099	GGCCGGGAGGC TCCATGCCGCGG CGC[G/gap]GGAA GACGCTGTTATT TCTCCGGAG	G	gap			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1585	cg43958670	3101	CCGGGAGGCTC CATGCGCGGCG CGG[G/gap]AAGA CGCTGTTATTTC TCCGGAGGA	G	gap			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1586	cg44034752	1702	TAGGTTGACAAC TTGTCATGATTTT [G/A]ACGGTAAG CCACCATGATTG TGTTC	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z-GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1587	cg44034752	1763	TTGACCTTACAA AAACCATTGGAA C[gap/C]TGTGAC TTTGAAAGGTGC TCTTGCT	gap	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z-GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1588	cg44034752	1801	GGTGCTCTTGCT AAGCTTATATGT G[gap/G]CCTGTT AATGAAAGTGCC TGAAAGA	gap	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z-GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1589	cg44034752	1815	GCTTATATGTGC CTGTTAATGAAA G[gap/G]TGCCTG AAAGACCTTCCT TAATAAA	gap	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z-GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1590	cg34243197	2123	GCTTTCCTGGGC CTCTCAGTTGAA C[gap/C]AAAGCA GCAAAACAAAGG CAGTTTT	gap	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:Q61207 SULFATED GLYCOPROTEIN 1 PRECURSOR (SGP-1) (PROSAPOSIN) - MUS MUSCULUS (MOUSE), 557 aa.	5.00E-202	10 (10q22.1)

1591	cg43059879	106	GAACAAGAAACA AGTGTGACATTT T[A/G]TGTGGAAT CTGAAAACCACC TTAGC	A	G		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.|pcls:SWISSPROT-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.|pcls:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa	6.60E-199	17 (17q23)
1592	cg43932434	606	CTTTAAAGAACA AAACACAAAAAA C[T/A]TTAAGAGT AGAAAATTTTAT GCTAA	T	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)

1593	cg43932434	607	TTTAAAGAACAA AACACAAAAAAC T[T/A]TAAGAGTA GAAAATTTTATG CTAAA	T	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
1594	cg43932434	608	TTAAAGAACAAA ACACAAAAAACT T[T/A]AAGAGTAG AAAATTTTATGCT AAAA	T	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
1595	cg43988092	636	AATGCTTTTTAG AGCCTTTCTGTA G[C/A]GATACAAA TATATATATATAT ATTT	C	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.00E-192	8
1596	cg43988092	775	GTAAGACTATTT ATCCACCTGAAT T[C/T]TCAATTTC TTTAAAGTTAGT GCATT	C	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.00E-192	8

1597	cg43115790	122	GGTGGTTCTGAC TACAAGGGCTAG G[C/gap]CCTAGG ACATCTGGTTTT CTTTCTT	C	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q03395 ROD OUTER SEGMENT MEMBRANE PROTEIN 1 (ROSP1) - HOMO SAPIENS (HUMAN), 351 aa.	1.40E-191	11 (11q13)
1598	cg43918166	985	AAAATTTCTTTTTT TTTTTTTTTTTTT[T/gap]TTTTTTTGCA TGTGTTTTAACA ATC	T	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1599	cg43918166	986	AAATTTCTTTTTT TTTTTTTTTTTTT[T/gap]TTTTTTTGCAT GTGTTTTAACAA TCC	T	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1600	cg43918166	987	AATTTCTTTTTTT TTTTTTTTTTTTT[T/gap]TTTTTTGCAT GTGTTTTAACAA TCCC	T	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1601	cg43918166	992	TTTTTTTTTTTTT TTTTTTTTTTTTT[gap/T]GCATGTGTT TTAACAATCCCC CACC	gap	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5

1602	cg43918166	992	TTTTTTTTTTTTTTTTTTTTT[gap/T]GCATGTGTTTTAACAATCCCCCACC	gap	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1603	cg43918166	199	AAAATAGAAACCTACTAGATCAACA[C/A]AGTGTTGTTCTGTGCTCTAAAATAC	C	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1604	cg43918166	274	AACAACCAAGGGAACCTGCTTAAAC[A/G]TACTGTGTATTATTGTAGCTAGAGT	A	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1605	cg43918166	310	TATTGTAGCTAGAGTCATTCCTTCT[A/T]AGCCAAAGGAGGTTTTATAAAAAAG	A	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1606	cg43918166	334	AAGCCAAAGGAGGTTTTATAAAAAA[gap/A]GAATCAATATTGGGCCAATCCCTTT	gap	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5

1607	cg43918166	3444	ATTCCTCACTTG ATGGTTTGAAAG T[C/T]GCTTCAAT ATTTACATGAATT TCCT	C	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1608	cg43918166	968	AAAATGGTTATA TATACAAAATTTC [T/gap]TTTTTTTTT TTTTTTTTTTTT TTTG	T	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1609	cg44022653	246	TATAACCCTTTC ATACTAGTTGAA C[gap/T]TTTTTTT TTATAATGTACAT GTACT	gap	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1610	cg44022653	247	TATAACCCTTTC ATACTAGTTGAA C[T/gap]TTTTTTT TATAATGTACAT GTACTA	T	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1611	cg44022653	255	TTTCATACTAGTT GAACTTTTTTTT T/gap]ATAATGTA CATGTACTACTT TATAA	T	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1612	cg44022653	258	ATACTAGTTGAA CTTTTTTTTATA[gap/T]ATGTACAT GTACTACTTTATA ATTA	gap	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1613	cg44022653	280	TATAATGTACAT GTACTACTTTATA [A/G]TTAAACAAA AAACTTTAAAAT GATT	A	G		SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

1614	cg44022653	323	AATGATTTTTTAAAAAAGAAAAGAA[gap/G]TTAATCACAGTGGAACATGAAATGG	gap	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1615	cg44022653	357	GTGGAACATGAAATGGAATGTCAAC[gap/G]TTTGGGGACGGGTCATCCAGAGGAG	gap	G			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1616	cg44022653	367	GAAATGGAATGTCAACTTTGGGGAC[G/A]GGTCATCCAGAGGAGTCCAAGAGCC	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1617	cg44022653	401	AGAGGAGTCCAAGAGCCCCAACATG[G/T]TCGCGTGTCTCTGGTCCTCAGGTCA	G	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1618	cg44022653	414	AGCCCCAACATGGTCGCGTGTCTCT[G/T]GTCCTCAGGTCATCACCCAGCCTCA	G	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1619	cg44022653	421	ACATGGTCGCGTGTCTCTGGTCCTC[A/T]GGTCATCACCCAGCCTCACCCACAG	A	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1620	cg44022653	496	CCGTGCAAGCTTCCACTTGGTGCCT[G/A]CGTGGGAACGCACCACCTGCCGTGG	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

1621	cg44022653	498	GTGCAAGCTTCC ACTTGGTGCCTG C[G/A]TGGGAAC GCACCACCTGCC GTGGAA	G	A			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1622	cg44022653	654	CCCTCCCACGCA GTGTGAGCCCTG G[G/gap]CTGCGC CACACCCGCAG GTGGCCCG	G	gap			SILENT-NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1623	cg43318219	1858	TTTTTCAAGAAAA CTGGAAATCTGG [A/T]TTTTCAGCG AACATGCCTGAT TTTA	A	T			SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P15813 T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa.lpcls:SWISSPROT-ID:P15813 T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa.	3.10E-185	1 (1q21)
1624	cg40915005	1796	GGTCCTAGCAAC CTCCACATGTTC A[A/C]CTATTAAT GGATCATCAGGC CTGTT	A	C			SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.lpcls:SWISSPROT-ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (1q21)

1625	cg4358915	205	GTAGATTTAACC ACAGAACTGTCT C[G/A]ATTTTTAT AAAAATTGATCC CAAGA	G	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.|pcls:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11
1626	cg4358915	331	CCCAAAGGGGA GAGGTGTGGGG CGG[C/T]GGGGC GGGGAGGCGCC TTGTGCTGT	C	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.|pcls:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11

1627	cg43958915	346	TGTGGGGCGGC GGGGCGGGGAG GCG[C/gap]CTTG TGCTGTGGCACT GGACACGGT	C	gap		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.|pcls:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11
1628	cg43958915	387	TGGACACGGTG CTCATCTGCAGG AT[G/A]GCCACG AAGACAAACGGC ACAGACG	G	A		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.|pcls:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11

1629	cg43977071	1845	TGCAGGTTAGGT TCCAGACCACTT A[G/T]GAGTCTGC GAAACGCCCAC GCTCCA	G	T		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P28328 PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) (35 KD PEROXISOMAL MEMBRANE PROTEIN) - HOMO SAPIENS (HUMAN), 305 aa.|pcls:SWISSPROT-ID:P28328 PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) (35 KD PEROXISOMAL MEMBRANE PROTEIN) - HOMO SAPIENS (HUMAN), 305 aa.	1.20E-169	8 (8q21.1)
1630	cg43124001	1942	CAGGGGATTTTA TCCCCCACCAAA A[A/G]CACAGTGA AAGGCCTGCTTT TGTGT	A	G		SILENT-NONCODING	glycoprotein	Human Gene SWISSNEW-ID:O42281 PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) (PHOTORECEPTOR OUTER SEGMENT MEMBRANE GLYCOPROTEIN 1) (CRDS1) - GALLUS GALLUS (CHICKEN), 354 aa.|pcls:SWISSPROT-ID:O42281 PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) (PHOTORECEPTOR OUTER SEGMENT MEMBRANE GLYCOPROTEIN 1) (CRDS1) - GALLUS GALLUS (CHICKEN), 354 aa.	5.50E-156	6 (6p21.1)
1631	cg43248459	577	CACAGAGAGGAT GAGAAACAAAAA A[A/gap]GAGAAA AGGAAAAGTAGG TTGAAGA	A	gap		SILENT-NONCODING	glycoprotein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	7.10E-155	20
1632	cg43248459	85	AACAGAGAGCAC ACGCATACAGCA C[G/A]GAGCACT GAGGTGGGGGA GCATGGG	G	A		SILENT-NONCODING	glycoprotein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	7.10E-155	20

1633	cg43953517	2391	AATAAAAATTTAT TGAGTGAAACAA[A/T]AAAAATACAA TGACTAGTCATG CAT	A	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.90E-150	4
1634	cg43953517	2396	AAATTTATTGAGT GAAACAAAAAAA[A/G]TACAATGAC TAGTCATGCATC ATCA	A	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.90E-150	4
1635	cg43922980	3766	TTATTTATTACAA AATTATATTCAC[C/G]TAAATGCCA ACCATCTACAAA AACA	C	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P97449 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13) (P161 MEMBRANE PROTEIN) - MUS MUSCULUS (MOUSE), 965 aa.	2.00E-135	5
1636	cg43922980	3957	AGGCCGCTGGTT TGTCAGCCATCT G[T/C]TGCTTCTT ATTGATAGATGG CATTG	T	C			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P97449 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13) (P161 MEMBRANE PROTEIN) - MUS MUSCULUS (MOUSE), 965 aa.	2.00E-135	5
1637	cg43951991	152	TTACGCACCGCA TGAGAACCGTTA G[gap/G]TTATAA AATCTATCATCA ACCAGTA	gap	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1638	cg43951991	27	TTTTTTTTTTTTT TTTTTTTTTTC[C /T]TTTATCAATG TTTTATTTTTAAA A	C	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1639	cg43951991	836	ATATTTTAACAAA GGAAAAAAAAA[gap/A]GCAACATT CACAGCACATCA AGCCC	gap	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	

1640	cg43951991	881	AAGCCCAAAATAGTTTACACCTTCT[A/T]CACTGAAGCATTGTTTAAAATGTAC	A	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1641	cg43948148	88	GTTTCTTTAAAAATAAAAACCCCAC[gap/A]AAAAAAGCCAGAACACCCTACCCAA	gap	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01650 INTEGRAL MEMBRANE PROTEIN E16 - HOMO SAPIENS (HUMAN), 241 aa.	2.00E-128	16
1642	cg44004667	2076	AAAGAAAATCTCTGTGAAACCCCTA[T/C]GTGGAGGCGGAATTGCTCTCCCAGC	T	C			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.|pcls:SWISSPROT-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	
1643	cg44004667	2296	GAGCCCCTCACACAGCCCTGGCCTC[T/C]GCTCAACTAGCAGATACAGGGATGA	T	C			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.|pcls:SWISSPROT-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	

1644	cg43301424	1194	TGCCCCACCTCC TAACCTAATCCC C[C/A]CGCCCCG CTGCCTTTCCCA GGCTCC	C	A			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.|pcls:SWISSPROT-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM-ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.	2.30E-125	19 (19q13.2)

1645	cg43301424	1228	TGCCTTTCCCAGGCTCCCCTCACCC[C/gap]AGCGGGTAATGAGCCCTTAATCGCT	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.|pcls:SWISSPROT-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM-ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.	2.30E-125	19 (19q13.2)
1646	cg42852276	1537	AAAGGCATTATTCTCCAGCCTTAAG[gap/T]ATCTTAGGACGTTTCCTTTGCTATG	gap	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P26718 NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 216 aa.|pcls:SWISSPROT-ID:P26718 NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 216 aa.	5.70E-122	12
1647	cg43068999	874	TGGATACTAGATCTTACATCTGCAG[C/gap]TCTTTCTTCTTTGAATTTCCTATCT	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P02743 SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 223 aa.	1.60E-119	1 (1q21)

1648	cg43986150	1655	ATAAAACAGTTTATTATCTCAATCA[A/C]AACATTCCTATATATCAAACACTCC	A	C			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P19397 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53) - HOMO SAPIENS (HUMAN), 219 aa.	2.60E-117	1 (1p21)
1649	cg43986150	206	CTCGGCCACCTCAAGGATAATCACT[G/A]AATTCTGCCGAAAGGACTGAGGAAC	G	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P19397 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53) - HOMO SAPIENS (HUMAN), 219 aa.	2.60E-117	1 (1p21)
1650	cg44018623	203	TATTTTATAATAGTATTACAGGAAG[C/A]AAAATATCATTTAATACAACTTGAG	C	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.90E-114	6
1651	cg43051796	1421	TGGCCAGAGAGTCCTTGTAATTGTC[C/T]CCAATTCAATCAGTATTTTGGGGCT	C	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.|pcls:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3
1652	cg43051796	259	ACAACAAATAACAATACTTAGGATA[C/A]ATCAATCATTCTTTTTCCTCTTAAA	C	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.|pcls:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3

1653	cg43051796	286	TCAATCATTCTTTTTCCTCTTAAAA[A/T]CAGAAATTGGTCTTAGTTTCTCATT	A	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.|pcls:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3
1654	cg43287997	1244	CCCTCCTTTTCTTGCATGTAAGTTG[gap/G]TCCCCCATCCCAAAGTATTCCATCT	gap	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1655	cg43287997	1430	ACCCCCTAATCCCCTACTCCCTCCA[gap/A]CCCCCCCTCCACTGTAGGCCACTGG	gap	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1656	cg43287997	1440	CCCCTACTCCCT CCACCCCCCCTC C[gap/C]ACTGTA GGCCACTGGAT GGTCATTT	gap	C		SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1657	cg43287997	1466	CTGTAGGCCACT GGATGGTCATTT G[gap/G]CATCTC CGTAAATGTGCT CTGCTCC	gap	G		SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1658	cg43287997	1477	CTGGATGGTCAT TTGCATCTCCGT A[A/T]ATGTGCTC TGCTCCTCAGCT GAGAG	A	T		SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1659	cg43287997	1487	TTTGCATCTCCG TAAATGTGCTCT G[gap/G]CTCCTC AGCTGAGAGAGA AAAAAT	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1660	cg43287997	903	GCCTGAATCAGA GACGCATCTGAC C[C/gap]TCTGGA GAACACTGCCTC CCGCTGG	C	gap		SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1661	cg43287997	906	GAATCAGAGACG CATCTGACCCTC T[gap/T]GGAGAA CACTGCCTCCCG CTGGCCC	gap	T		SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1662	cg43924574	155	GGCTTGGAAGAGAGATCCAAAGGCC[A/G]GCCTGGCAAGGGGAATCCCACATGA	A	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.|pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	1.00E-106	1
1663	cg41598396	225	CAAAGCTGGGACTGGAGGGGCTTTA[G/gap]CGACTCAATTCCAGGTGCAGCATTT	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.|pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	4.50E-106	1
1664	cg43917157	1386	GGTGAAACTGTCACAATCCGTGTCC[C/A]TTTTATATATAACTATACTGAGGTA	C	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1665	cg43917157	1545	CACGCAATCTGCTTGGGACAAAAAG[C/T]CTACAGGGGTTGCCAAGCACGAAAG	C	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6

1666	cg43917157	1650	GGAACTCCATAAAAGAATGAGGCAG[C/T]TTTCACTGGGGAGAACTGGTCTTCA	C	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1667	cg43917157	21	TTTTTTTTTTTTTTTTTTTTTTT[T/G]TTAATTTTCTGCCTTTTATTGTTAT	T	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1668	cg43917157	222	TTTTTTACATGAAAGCATAAATACG[G/A]CAGGTACAAATTTTCCTTGAGTTCC	G	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1669	cg43917157	3218	GGGAAGCAGAGCCTAAGCTGACCCC[G/A]GCCACTGGGCTGGTGGGACCACATC	G	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1670	cg43917157	3305	AGAGACAGGGACATGAAGTTGTGGC[G/A]TCTCTGGCACGCAAGTGTCCTGGGA	G	A			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1671	cg43917157	3322	GTTGTGGCGTCTCTGGCACGCAAGT[G/gap]TCCTGGGACAGAGCAATGGAAACCT	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6

1672	cg43917157	4330	TGCCTGCCACTACACCTAATTTTTT[T/gap]GTATTTTTAGTAGAGATGGGGTTTC	T	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1673	cg43917157	776	TGGCTATTTCTTGTGTAAGGGATGA[C/T]GACTCCCCCTCCCATGGGTCCCATT	C	T			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1674	cg43255952	160	AACGGGCTGAGAAGGCCCGTCAGGG[gap/G]CCCAGGTCCCACAGAGAGGCCTGGG	gap	G			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.|pcls:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
1675	cg43255952	226	GAGGGGCAGACTGGGCAGTGGGGAG[C/gap]CCCCATCGTGCCCCAGAGGTGGCCA	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.|pcls:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)

1676	cg43255952	373	AAAAGCACCAG GTCAGGCAGGG CC[C/gap]GAGGG CCCCAGATCCCA GGAGGGCC	C	gap		SILENT-NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.|pdb:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
1677	cg43094350	507	ACCAAAAATACC CCTCTCTCCCCA C[A/T]CCTCTTCT CCGACCCTCCG GGAGGC	A	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	5.4E-95	7
1678	cg43094350	715	CAGGATGGTGTG TAGCCCAGTGAC T[C/G]TGAGGATC GCCCCTCCTGAC AGAAG	C	G		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	5.4E-95	7
1679	cg36834323	24	CAGGGAAGCTC CAGCTGTCCCTC [G/C]CGCAGTTG GCCCTGTGGTGT TCCGA	G	C		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.4E-91	
1680	cg43054905	341	ATCCAATGATCA GCGTGAGATGAT C[A/T]TTGATTAA ACTTGCTTGAGA TGGCT	A	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.1 1)

1681	cg43054905	382	TGAGATGGCTAGTCAAACGTCGAAA[G/C]TTGCTTGAGATGGCTAGTCAAACGT	G	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.11)
1682	cg43054905	454	TAACTAGACTTTTACAATTTTTTTT[gap/T]AAAGGGTAAAAAGACATGAACCCTA	gap	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.11)
1683	cg43949899	236	TCCCATTTTTATTTTTTTTTTTTT[G/T]AGTATTCAATGAATGGAATTTAATG	G	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P20172 CLATHRIN COAT ASSEMBLY PROTEIN AP50 (CLATHRIN COAT ASSOCIATED PROTEIN AP50) (PLASMA MEMBRANE ADAPTOR AP-2 50 KD PROTEIN) (HA2 50 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 MEDIUM CHAIN) (KIAA0109) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 435 aa.	1.1E-84	19
1684	cg44021513	202	GTCCGCTGGGCAGTTATAGGTCCCA[A/T]GTGTTGGGTCTTCCTGCGAGGCCTT	A	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
1685	cg44021513	209	GGGCAGTTATAGGTCCCAAGTGTTG[G/C]GTCTTCCTGCGAGGCCTTCACAAAG	G	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)

1686	cg44021513	319	ACTTTATTCACA CTGTGTAACCAC A[gap/C]TGTTTTT TATGCCACTTTG TGCACA	gap	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
1687	cg44019290	969	GTGCCCTCACAT CTGGGGTCTTCA G[G/gap]CACCAG CCATGCCTGCCG AGGAGTG	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1688	cg44019290	1029	CAGACCATGTCC GTGCTAGGCCCA G[G/gap]CACAGC CCAACCACTCCT CATCCAA	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1689	cg44019290	1380	CTTCTCCTCAAG GTTTGAGGGATT G[C/G]GGGGAGG GGGTCAGCTGA CTCAGAG	C	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1690	cg44019290	411	TCCTGGGTCTCA CTCCATGGCTTG C[C/gap]TCAGGC CCCGCAGAAGTC CCTGAGA	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1691	cg44019290	773	TACCTCCTTCTC CAACCCTCCACT A[G/gap]CGCTGC TTTCCTGGTCAA ACCTGCA	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11

1692	cg42876034	122	CTGGGGCAGCA CCACCTGAAGGC AG[T/C]GACTGC CTTTTTAAAAGA CAGGGTT	T	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa.	2.6E-78	
1693	cg41672027	1002	GCATCATTTAATT GCGACATACCAG [G/T]GGAAATTGT ATGTATGTTAGT GACA	G	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q03401 SPERM-COATING GLYCOPROTEIN 1 PRECURSOR (SCP 1) (ACIDIC EPIDIDYMAL GLYCOPROTEIN 1) (CYSTEINE-RICH SECRETORY PROTEIN-1) (CRISP-1) - MUS MUSCULUS (MOUSE), 244 aa.	3E-77	6 (6p21)
1694	cg43919735	302	AATTCTCACTCT ATCCAAAGCCCC G[G/gap]ATGAGG TCACTGCTTTTAT GAGCCT	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P08962 CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP 3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) (GRANULOPHYSIN) - HOMO SAPIENS (HUMAN), 237 aa.|pcls:SWISSPROT-ID:P08962 CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP 3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) - HOMO SAPIENS (HUMAN), 237 aa	2.2E-76	11 (11q12)

1695	cg43981337	1111	GATTGAATCAGCCCACTGCGAGCAC[G/A]GATCTTGATTGAATCAGCCTATTGG	G	A			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.9E-75	X
1696	cg43981337	1146	TGAATCAGCCTATTGGTGTAGTTTT[A/G]GGTCTACATACATCTTGATTGAATC	A	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X

1697	cg43981337	1256	GCAACTTTCTAATTCACAGGGGGGA[C/gap]CCTAAATGTCCTTAAAGGTAGAGAG	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X
1698	cg43981337	1258	AACTTTCTAATTCACAGGGGGGACC[C/gap]TAAATGTCCTTAAAGGTAGAGGA	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X

1699	cg43981337	567	CTCAATTTGGAGGCAAAGAAATGTA[A/G]GTTGTGTGCTGAAACCTGATGTATC	A	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X
1700	cg43983795	1810	CGCCGCTCTCCAGATCGCTTGGGTC[G/gap]CGCCAGTCGCCACCACATCCTCGGC	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X
1701	cg43983795	1810	GCCGCTCTCCAGATCGCTTGGGTCG[gap/G]CGCCAGTCGCCACCACATCCTCGGC	gap	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X
1702	cg43983795	45	TTTTTTTTTTTTTTTTTTTTTTT[A/T]GTGGGTAAAACCATTTTTATTAACT	A	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X

1703	cg41602760	1820	GCCCACTGAGAAGAGCTTCCAGGAC[G/gap]CACCCAGGACGCTGAGCCCAGGAGC	G	gap		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	3.40E-73	15 (15q26.1)
1704	cg41568631	143	GATGTGGGCCGTTGGGGTGGCAACC[C/gap]CTTGCAGCCCCCTACCACGCCATCT	C	gap		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1705	cg41568631	144	ATGTGGGCCGTTGGGGTGGCAACC[C/gap]TTGCAGCCCCCTACCACGCCATCTC	C	gap		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1706	cg41568631	70	TCCATCTCAGCCCCAGGACTCAGTA[C/T]TGCGGTTGCCAACACTGCTGCCAGG	C	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1707	cg41568631	71	CCATCTCAGCCCCAGGACTCAGTAC[T/C]GCGGTTGCCAACACTGCTGCCAGGC	T	C		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1708	cg43918233	1667	TTATGCTGGTGGCTTCCATCCGTTC[C/gap]TCCTCTGAGGGTGAGTGGAGAGGTA	C	gap		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2

1709	cg43918233	1675	GTGGCTTCCATC CGTTCCTCCTCT G[A/gap]GGGTGA GTGGAGAGGTAT ATGGAAA	A	gap		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2
1710	cg43918233	1688	GTTCCTCCTCTG AGGGTGAGTGG AG[A/G]GGTATAT GGAAACACGGCT GTGACC	A	G		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2
1711	cg43918233	1708	TGGAGAGGTATA TGGAAACACGGC T[G/A]TGACCAAA GGGAGATCCCA GCCTGG	G	A		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1712	cg43918233	1738	CAAAGGAGATC CCAGCCTGGGC AG[G/C]CTGCGC TGCTGACCACCC TCCCTGG	G	C		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1713	cg43918233	1988	TCTTCAAAGACT TCAGCAGCAAAC C[A/T]AAACAGCA GGTTAAAAAAAA AGATG	A	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1714	cg43918233	319	GAAGACACCCCC AACAAGTCGGGT G[C/G]GGAGGCA AAGACCCAAAAA GACAGC	C	G		SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2

1715	cg43918233	334	AAGTCGGGTGC GGAGGCAAAGA CCC[A/T]AAAAGA CAGCTCCAACAA GTCGGGT	A	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1716	cg43918233	369	CTCCAACAAGTC GGGTGCGGAGG CA[A/C]AGACCCA AAAAGGCAGCAC TAGCAA	A	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1717	cg43918233	377	AGTCGGGTGCG GAGGCAAAGAC CCA[A/C]AAAGG CAGCACTAGCAA GTCGGGTT	A	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1718	cg43927045	1406	TAAAAAACGCGG CTGTGGAGACAG G[T/A]GAGCTGCT GGGAAGCCATGT TTTTG	T	A			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1719	cg43927045	1420	GTGGAGACAGG TGAGCTGCTGG GAA[G/gap]CCAT GTTTTTGATTTTC AGACAGGT	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1720	cg43927045	1556	ATCAATACACAA GAGACTCTTTGT G[G/A]CTCAACAC GTGGGGTCGCG AGGCAG	G	A			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1721	cg43927045	2176	GAACTGGCGGC CACGATGATGGA CT[G/gap]CCGCT GGCCCCGGAGG GTCAGGCAG	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13

1722	cg43927045	2184	GGCCACGATGAT GGACTGCCGCT GG[C/gap]CCCGG AGGGTCAGGCA GTGGGGCAC	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1723	cg43927045	2203	CGCTGGCCCCG GAGGGTCAGGC AGT[G/gap]GGGC ACCCCCCACTCG TCTTCGCTC	G	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1724	cg43927045	234	TTTGCAAGTTGC TGTTTGTTTCCA G[C/G]TACACCA GTCAGAGCTCCA CAGAGA	C	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1725	cg43927045	448	ACGTTTCCCGAG TAGGGGCCAAA GC[C/gap]ACTGG AAACCGTGTTCC CTGTGCAG	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1726	cg43927045	520	CCTGGGGGGAA TGAGTATAAAAA GG[G/T]AAATGTT TTTGAAGACAGG CACGAT	G	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13

1727	cg44014928	1879	GAGTGGAGCTTTAAGTAAATATGC C[A/gap]AAAAAATATTCCTAGCA CAAAAGC	A	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.|pcls:SWISSPROT-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5
1728	cg44014928	1886	GCTTTAAGTAAATATGCCAAAAAA A[A/gap]TATTCCTAGCACAAAAGCC TGCACC	A	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5

1729	cg44014928	2113	GAAAAGCAAAGCAAGAGAATTCTGC[T/C]AAGAAGTTTTATTCTGAATCTGAGG	T	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.|pcls:SWISSPROT-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5
1730	cg44024345	797	AGCTTTACTGCCTTCCTCCTTATCC[T/C]ACAGTACAATCAGCAGTCTAGTTCT	T	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.|pcls:SWISSPROT-ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.	7.70E-63	6
1731	cg44024345	848	TTTCATTTGGAATGAATACAGCATT[T/A]AGCTTGTTCCACTGCAAATAAAGCC	T	A			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.|pcls:SWISSPROT-ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.	7.7E-63	6
1732	cg43965366	773	CACTAACTAAAGAGATAAATTCTTC[gap/C]ACTTTACTTCCTAGTATTGCATCCC	gap	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)

1733	cg43965366	828	AGGGTTAAAGTAAGGGATATTGGCT[C/T]CTGCTGATCAGGCCACAGTGTGACA	C	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)
1734	cg43279524	926	CTCCCCGCCCCCCGTGTTGAGACAGG[T/G]TCTCAAGGCTCAGGGGAAGATGCAT	T	G		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSNEW-ID:P17426 ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) MUS MUSCULUS (MOUSE), 977 aa.|pcls:SWISSPROT-ID:P17426 ALPHA ADAPTIN (A) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) - MUS MUSCULUS (MOUSE), 977 aa.	2.8E-60	14
1735	cg43252235	1172	TTAAAGGATGGGGTCTTGCTATATT[gap/A]GCCCAGGCTGGAGTGCAGTGGCTAT	gap	A		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.8E-60	

1736	cg43252235	1172	TTAAAGGATGGGGTCTTGCTATATT[gap/A]GCCCAGGCTGGAGTGCAGTGGCTAT	gap	A			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1737	cg43252235	68	TTTTTTGAATGTAATATTTATTTGG[T/G]GAATTTACATGTGAGGTCATTTACA	T	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1738	cg43252235	848	AGACCTGGACCTGGGTAGTTAGTCC[C/T]TAGAGATGAAGGTGAGCTCACTACA	C	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1739	cg44965847	200	CAGTAGGCTCCCCCAGGCTGAGCCC[C/gap]AGCCCTAACACTGATGCTTGGCAGC	C	gap			SILENT-NONCODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q27127 P-GLYCOPROTEIN - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 302 aa (fragment).	2.60E-58	

1740	cg43322513	1069	GCTGTCCGATGG CGTGGAACACAA G[G/C]CCCCCCA CACGGAACATGT GCAGCC	G	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1741	cg43322513	11318	TTCCTGCAAGTA AGCAGGGAACAT G[T/C]CCTCCAGT TTGCTCTTCTTG CGCCC	T	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1742	cg43322513	11333	AGGGAACATGTC CTCCAGTTTGCT C[T/C]TCTTGCGC CCTCGCCGCTGT TGCTT	T	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1743	cg43322513	11379	TGCTTCTTCTTCT CATCCCCTTCAG[G/C]CAAGCTCTG CTCCACGGCGC CCTCT	G	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1744	cg43322513	1268	CATGCACTTGGC ACGGATGGCACA A[G/C]CAAAATGG TAGACATTGGGG CAACG	G	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1745	cg43322513	1390	GGGCAACCTCCA CATTCATCAGTG C[C/T]CCGCCCT GGGTCTCATACA CCTCCG	C	T			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.3E-54	12

1746	cg43322513	8482	AGCTGCCTGGA GGCCCCACTGCT CC[T/C]GCAGCT GCTGCAGCTGTT TCCTTCT	T	C		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.3E-54	12
1747	cg43982558	1399	CAACTGAATGTG CCCTTAGAGCGC A[T/C]CAGTTTTA AAGTCATTAAGA ACATG	T	C		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.1E-53	5 (5q13)
1748	cg43982558	1400	AACTGAATGTGC CCTTAGAGCGCA T[C/T]AGTTTTAA AGTCATTAAGAA CATGT	C	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.1E-53	5 (5q13)
1749	cg43982558	1443	GAACATGTGAAA GGTGTTTTTTTTT [T/gap]CCAATAT GAACTCATGCAA GTTACC	T	gap		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1750	cg43982558	1653	AGCTGTATCATC CCAACAAAGTAT C[C/T]TTTCATGA ACGGGGCATGC AATAGC	C	T		SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)

1751	cg43982558	218	CTTAAGGTGAGGAGAAAGAGCGCTA[G/C]CTTCACTTGATCTCCAGCTTCCAAC	G	C			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1752	cg43982558	219	TTAAGGTGAGGAGAAAGAGCGCTAG[C/G]TTCACTTGATCTCCAGCTTCCAACT	C	G			SILENT-NONCODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1753	cg43937369	378	GGCCAAGAAGGGCTCTAACAGCAGT[A/G]TCCCAGCAGTGTGTTTCCAGATTTA	A	G			SILENT-NONCODING	Guanylyl	Human Gene SWISSNEW-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.|pcls:SWISSPROT-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	4
1754	cg43937369	424	ATTTATTCTTGGATGTGGTTGGAGC[G/T]CCCAACATTTAGCCTGAACTAATGT	G	T			SILENT-NONCODING	Guanylyl	Human Gene SWISSNEW-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.|pcls:SWISSPROT-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	4

1755	cg42716105	484	GAGTCCTTATAC CTCATTTAGGTT T[gap/A]AAAATAG GTGCTCTCCTTG TCTGTG	gap	A			SILENT-NONCODING	Guanylyl	Human Gene SWISSPROT-ID:P25092 HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) - HOMO SAPIENS (HUMAN), 1073 aa.	0.00E+00	12
1756	cg43069304	129	TCTAGCATTAGT ACATAGTAGGCG C[gap/C]TCAGTA AATGCTTGTTGA AGGGAGG	gap	C			SILENT-NONCODING	Guanylyl	Human Gene Homologous to SWISSPROT-ID:P43080 GUANYLATE CYCLASE ACTIVATING PROTEIN 1 (GCAP 1) - HOMO SAPIENS (HUMAN), 200 aa.	8.40E-105	6
1757	cg42905276	2266	AAGGAAGCCCC CCACTTTTTTTTT T[gap/T]CTGCCT GAGATTCTTTAA GGAGATA	gap	T			SILENT-NONCODING	Guanylyl	Human Gene Similar to SWISSPROT-ID:P16066 ATRIAL NATRIURETIC PEPTIDE RECEPTOR A PRECURSOR (ANP-A) (ANPRA) (GC-A) (GUANYLATE CYCLASE) (EC 4.6.1.2) - HOMO SAPIENS (HUMAN), 1061 aa.	1.20E-51	
1758	cg44913214	2375	GATTCGGACTAG TTTTCTGTTCCT G[T/gap]CTTTTTT TTTTTATTTAATT TTGCA	T	gap			SILENT-NONCODING	helicase	Human Gene TREMBLNEW-ID:G2801555 PUTATIVE ATP-DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
1759	cg44913214	2387	TTTTCTGTTCCT GTCTTTTTTTTTT[T/gap]ATTTAATTT TGCAAATAAAAA TTTA	T	gap			SILENT-NONCODING	helicase	Human Gene TREMBLNEW-ID:G2801555 PUTATIVE ATP-DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
1760	cg43956596	4029	AGGATGGCAGC AGGTATTGGGTC CT[G/C]AGCCTTC TGGCGGGAGCC CTGAGGC	G	C			SILENT-NONCODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.|pcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16

1761	cg43956596	4158	CTCTCTGGCAGA GGAGGTGGAGT TC[T/C]TCCATGC AGGAGCACGGC ATGGCGG	T	C		SILENT-NONCODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.|pds:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16
1762	cg43931763	105	TTGAGCTGTGGG GAGGTTCCAGCA G[T/C]AGCTACAG TGACGACTAAGA CTCCA	T	C		SILENT-NONCODING	helicase	Human Gene TREMBLNEW-ID:G2306766 ZINC FINGER HELICASE - HOMO SAPIENS (HUMAN), 2492 aa.	0.00E+00	X
1763	cg43937443	306	TCAACAAACAAA CTACACGTCTTT T[A/T]TTCGGTGT AATACTTTATTTT CTAT	A	T		SILENT-NONCODING	helicase	Human Gene SWISSNEW-ID:Q08211 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) - HOMO SAPIENS (HUMAN), 1270 aa.|pds:SPTREMBL-ID:Q99556 NUCLEAR DNA HELICASE II - HOMO SAPIENS (HUMAN), 1270 aa (fragment).	1.90E-189	1
1764	cg43937443	399	AAATCTTTACTC CTTAAAGAAAAA A[gap/A]TACAAA CTGTGGTATTTT TAAGAGA	gap	A		SILENT-NONCODING	helicase	Human Gene SWISSNEW-ID:Q08211 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) - HOMO SAPIENS (HUMAN), 1270 aa.|pds:SPTREMBL-ID:Q99556 NUCLEAR DNA HELICASE II - HOMO SAPIENS (HUMAN), 1270 aa (fragment).	1.90E-189	1
1765	cg43924685	497	CTTTTATACCCA CCCCAACAGTCT A[A/G]CTCTAAAG AGGATAAAGCCA ATGAC	A	G		SILENT-NONCODING	helicase	Human Gene Homologous to SWISSPROT-ID:Q12099 PROBABLE ATP-DEPENDENT RNA HELICASE FAL1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 399 aa.	9.40E-121	3 (18p11.2)

1766	cg43329991	20	TGCGGCCGCCG TGCTGCCG[C/ga p]GCACTCTGGG CTGCTCTGGGC GCTG	C	gap			SILENT-NONCODING	helicase	Human Gene Homologous to SWISSPROT-ID:Q14147 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0134 - HOMO SAPIENS (HUMAN), 576 aa.	6.10E-102	19
1767	cg43958815	437	ATTCTGTTGTCA AGGGGCAAGAT GC[C/gap]AGCTT GGAAGTGCCAA GGAGCTAAA	C	gap			SILENT-NONCODING	helicase	Human Gene Similar to SWISSPROT-ID:Q06218 PROBABLE ATP-DEPENDENT RNA HELICASE DBP9 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 594 aa.	3.90E-100	
1768	cg43969995	1606	TACTAAATAAAA CCCATCAGTTTT T[T/G]TTATGTA GAAAAGCAATTT ATTCC	T	G			SILENT-NONCODING	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.|pcls:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.90E-214	
1769	cg43969995	1607	ACTAAATAAAAC CCATCAGTTTTTT [T/G]TTATGTAGA AAAGCAATTTATT CCA	T	G			SILENT-NONCODING	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.|pcls:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.90E-214	

1770	cg43969995	1903	CCAAGTTAAAAA AAAAAAAAAAAA A[A/gap]CCAACA ACAAAAAAAAAA ACACCAT	A	gap		SILENT-NONCODING	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.|pcls:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.9E-214		
1771	cg43969995	3855	CCATGGCGGGC AGGCGAGCCGG GGG[A/gap]ATCC TGGGGTCGAGC GTTGCGGGAG	A	gap		SILENT-NONCODING	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.|pcls:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.9E-214		
1772	cg44026400	225	TTGGGTTTTAGA AGTAGGCGTTCG C[C/gap]TATTTCT TCTTGGGCGCC GCCTTCT	C	gap		SILENT-NONCODING	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
1773	cg43948414	725	CCCCCTCCCGCA GCTACAACTACT T[A/T]TAATAAAG GACTCAAAAAGA GATCG	A	T		SILENT-NONCODING	histone	Human Gene Similar to SWISSPROT-ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	

1774	cg43948414	726	CCCCTCCCGCA GCTACAACTACT TA[T/A]AATAAAG GACTCAAAAAGA GATCGG	T	A			SILENT-NONCODING	histone	Human Gene Similar to SWISSPROT-ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1775	cg43948414	729	CTCCCGCAGCTA CAACTACTTATA A[T/A]AAAGGACT CAAAAAGAGATC GGGAG	T	A			SILENT-NONCODING	histone	Human Gene Similar to SWISSPROT-ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1776	cg43948414	772	ATCGGGAGGTTT TAAGTGGCCGCA G[C/gap]CCCACC AAACCAAGCAAA GACACCT	C	gap			SILENT-NONCODING	histone	Human Gene Similar to SWISSPROT-ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1777	cg43250123	8190	AGCGAGCGCCG CCCGCCCTCACT GG[C/T]CTTGTGA CGGTTTATTCTG ATTGAG	C	T			SILENT-NONCODING	histone	Human Gene Similar to SWISSPROT-ID:P53973 HISTONE DEACETYLASE HDA1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa.	2.4E-57	
1778	cg43918434	147	TAATTCAGTTAT GGTAAAAAAAAA A[A/gap]CTATGTA CATCTCAATCAG ATCACG	A	gap			SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1779	cg43918434	434	ACAGAAATCATT TTAAAAAGGGGA A[G/gap]GAGTTT TGTGTTGGAATC AATTGTG	G	gap			SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1780	cg43918434	435	CAGAAATCATTT TAAAAAGGGGAA G[G/gap]AGTTTT GTGTTGGAATCA ATTGTGC	G	gap			SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21

1781	cg43918434	437	GAAATCATTTTAAAAGGGGAAGGA[G/gap]TTTTGTGTTGGAATCAATTGTGCTA	G	gap			SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1782	cg43918434	454	GGGAAGGAGTTTTGTGTTGGAATCA[A/G]TTGTGCTACCTCTGTAAAAATGAAG	A	G			SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1783	cg43918434	592	TCTGCGGCAAGGCACCTGGTCTGCC[C/gap]TCCGGACAGCCTTTCGCCCAGTCTT	C	gap			SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0.00E+00	21
1784	cg42341753	2020	TGGAGCCTACCTCCCGACATTCACG[C/gap]TTCGCCCCACGCTGCTCCGACTGGC	C	gap			SILENT-NONCODING	homeobox	Human Gene SWISSPROT-ID:Q14774 HOMEOBOX PROTEIN HLX1 (HOMEOBOX PROTEIN HB24) - HOMO SAPIENS (HUMAN), 488 aa.	5.20E-263	1
1785	cg43918574	415	TCACTCAGAGGCCAAAGTCTGGGGG[T/G]TAGAAAGAAGGAAGCTTGACCCAAA	T	G			SILENT-NONCODING	homeobox	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.|pcls:SWISSPROT-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2
1786	cg43918574	453	AGCTTGACCCAAACAAAGTTTCAT[T/G]ACAGTATATACAGTCAGGCCTTGGG	T	G			SILENT-NONCODING	homeobox	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.|pcls:SWISSPROT-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2

1787	cg43918574	459	ACCCAAACAAAG TTTCATTTACAGT [A/G]TATACAGTC AGGCCTTGGGG GCAGG	A	G		SILENT-NONCODING	homeobox	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.|pcls:SWISSPROT-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245		2
1788	cg43988803	2504	ACAAAAAAAAAA ACCCTCCTTTTTTT [T/gap]CCTTTCGT CAGACTTGGCAG CAAAG	T	gap		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242	(13q14.1)	13
1789	cg43988803	3493	ATGTATGTATTTTT AAAGAAATTTCA[T/gap]CTGCTTCT ACTGAACTATGC GTACT	T	gap		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242	(13q14.1)	13
1790	cg43988803	3502	TTTTAAAGAAATT TCATCTGCTTCT[A/gap]CTGAACTA TGCGTACTGCAT AGCAT	A	gap		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242	(13q14.1)	13
1791	cg43988803	3590	CTCATAATGTTT GTAGATACAGAA A[A/gap]GGGAGA TCTGCATCTAAA GCAATGG	A	gap		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242	(13q14.1)	13
1792	cg43988803	3597	TGTTTGTAGATA CAGAAAAGGGA GA[T/gap]CTGCA TCTAAAGCAATG GTCCTTTG	T	gap		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242	(13q14.1)	13
1793	cg43988803	780	CACCGCAGCCC CCGCCGCCCGG GCC[G/C]CTGTC GCAGCACCCGC CGGTGCCCC	G	C		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242	(13q14.1)	13

1794	cg43988803	781	ACCGCAGCCCC CGCCGCCCGGG CCG[C/G]TGTCG CAGCACCCGCC GGTGCCCCCC	C	G		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242	13 (13q14.1)
1795	cg43986910	2486	GCCTTGAACAAA AAGTTTTTTTTTTT[T/gap]GTTTGTTT TTGCTTTCTGAA ATTCA	T	gap		SILENT-NONCODING	homeobox	Human Gene TREMBLNEW-ID:G2822167 HOMEOBOX PROTEIN HOX-A10 - HOMO SAPIENS (HUMAN), 415 aa.	1.40E-230	7
1796	cg44931625	1329	ACGGTAGCTAAC TTTGGGCAGGTT C[G/A]TTAAATTT GGTCAATTCAGA ACATT	G	A		SILENT-NONCODING	homeobox	Human Gene SWISSPROT-ID:P55347 HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1) - HOMO SAPIENS (HUMAN), 435 aa.	7.60E-230	21
1797	cg43027377	222	TGGCTTCTACCC AGAAAAAAAGG G[A/G]AGAGAGT ATAAAGAAGTGT CCAGAT	A	G		SILENT-NONCODING	homeobox	Human Gene SWISSPROT-ID:P40424 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEOBOX PROTEIN PBX1) (HOMEOBOX PROTEIN PRL) - HOMO SAPIENS (HUMAN), 430 aa.	5.70E-225	1 (1q23)
1798	cg43983917	1208	GTGCGGATCTG GCGGCCTACACA CG[C/gap]TGCGC TAAGCTGCAACG AAAACGAC	C	gap		SILENT-NONCODING	homeobox	Human Gene SWISSPROT-ID:P50458 HOMEOBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	
1799	cg43927965	1412	TTCAAGCAGGTA ACAATACTACTG G[A/gap]AAAAA AAATAGGAAGCT TAAAATG	A	gap		SILENT-NONCODING	homeobox	Human Gene SPTREMBL-ID:Q62947 ZINC FINGER HOMEODOMAIN ENHANCER-BINDING PROTEIN-1 - RATTUS NORVEGICUS (RAT), 1104 aa (fragment).	1.50E-207	
1800	cg43980506	1041	GCATGGAAAAGT TTTTATCTCTTCT [G/C]TTTCCTCTC CTGTAAGTAAAG ATTT	G	C		SILENT-NONCODING	homeobox	Human Gene TREMBLNEW-ID:G2896172 LIM HOMEOBOX PROTEIN COFACTOR - HOMO SAPIENS (HUMAN), 373 aa.	1.60E-206	

1801	cg43923014	1901	TGGCAGGGGTG AGGGCTGACGG GGG[A/G]ACAAC TTCAGCAGCTCA TGTCCCGA	A	G			SILENT-NONCODING	homeobox	Human Gene TREMBLNEW-ID:G2738116 LIM HOMEOBOX PROTEIN COFACTOR CLIM-2 - MUS MUSCULUS (MOUSE), 375 aa.	1.10E-203	
1802	cg43923014	457	CTGGGGGGGCA AATCTTGGCACC TG[C/gap]CCCCA GAGAGTCCAGTT CCTCCCTG	C	gap			SILENT-NONCODING	homeobox	Human Gene TREMBLNEW-ID:G2738116 LIM HOMEOBOX PROTEIN COFACTOR CLIM-2 - MUS MUSCULUS (MOUSE), 375 aa.	1.10E-203	
1803	cg42730678	692	AAGCACCAAACA CCCACAAAGGAA A[A/gap]CAGCAA CAACAACAAATC CGCTGCC	A	gap			SILENT-NONCODING	homeobox	Human Gene SWISSPROT-ID:P28356 HOMEOBOX PROTEIN HOX-D9 (HOX-4C) (HOX-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2
1804	cg43971616	516	CTCAGGGGGCA GTGGCCTGCTG CAG[C/gap]CTCT TGGCTTTTCCAC ATCTCCCAC	C	gap			SILENT-NONCODING	homeobox	Human Gene TREMBLNEW-ID:G2822168 HXAB_HUMAN HOMEOBOX PROTEIN HOX-A11 - HOMO SAPIENS (HUMAN), 313 aa.|pcls:TREMBLNEW-ID:G2745851 HOMEOBOX A11 - HOMO SAPIENS (HUMAN), 313 aa.	1.50E-169	7
1805	cg43926691	262	CAGAGGGTGGT GGCCTTTGGAAC CG[C/T]CGTGAA GTCTTCTGCCTG GAACCCG	C	T			SILENT-NONCODING	homeobox	Human Gene SWISSPROT-ID:P50222 HOMEOBOX PROTEIN MOX-2 (GROWTH ARREST-SPECIFIC HOMEOBOX) - HOMO SAPIENS (HUMAN), 303 aa.	2.00E-167	7
1806	cg43928699	1040	GGAGACCTTAAT TTTGACTTAACA A[A/gap]TAGTTTA TGTACTGCTCTT AGGTTG	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1807	cg43928699	1075	TACTGCTCTTAG GTTGTTTTGATA A[A/gap]GTGACA TTATAGTGATTAA ATTCTT	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10

1808	cg43928699	1080	TCTTAGGTTGTT TTGATAAAGTGA C[gap/G]ATTATA GTGATTAAATTC TTCCCCC	gap	G			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1809	cg43928699	1492	ACCTGTTTGACC AAGGTGTTAAGG G[G/gap]ATAGTA CCTCCCAATTCA AGCAGAG	G	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1810	cg43928699	1506	GGTGTTAAGGG GATAGTACCTCC CA[A/gap]TTCAA GCAGAGAAACTG ACCTGACT	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1811	cg43928699	1511	TAAGGGGATAGT ACCTCCCAATTC A[A/gap]GCAGAG AAACTGACCTGA CTAAAGT	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1812	cg43928699	1564	ATCGCAGATGAA CTAGAAGTCACA G[G/gap]TTAATTA AATGTAAGTAGA TTGTAG	G	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1813	cg43928699	1585	ACAGGTTAATTA AATGTAAGTAGA T[T/gap]GTAGATA CTGTTTTATATCA AACAA	T	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1814	cg43971192	191	GTATTGCACAGT CTGAAAAAATAA C[A/gap]AAAAA GGGAAGGGGAG GAAAAAA	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18

1815	cg43971192	210	AATAACAAAAAA AGGGAAGGGGA GG[A/gap]AAAAA AAAATCACATGA TATTGGGA	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1816	cg43971192	219	AAAAGGGAAGG GGAGGAAAAAAA AA[A/gap]TCACAT GATATTGGGAAC CATCTCA	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1817	cg43971192	50	ATACTTTATTATG TCATGAAAAAAA[A/gap]GGCATCAA CCAACTAGATTC ATACT	A	gap			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1818	cg43988027	16	CTTATTTTTTTTT TT[T/G]CTTTTT ATTGATTTTATTT CTCCG	T	G			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEOBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	5.50E-140	17
1819	cg42908326	1284	GAGTCTGGAGA GAGACTGGACA GGG[G/T]AGTGC TGGAACCGCGG AGTTTGGCT	G	T			SILENT-NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1820	cg42908326	1341	AAAGCTACAACG ATGGACTCTTGC A[C/T]AGAAAAAA AAATCTTGTTAA CAATG	C	T			SILENT-NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1821	cg42908326	1422	CAAACGGGAGA GAAAAAGAGGAA GG[A/C]AACTTAT TTCTTAACTGCT ATTTGG	A	C			SILENT-NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3

1822	cg42908326	2357	ATTCCCCTTTTCT[C/T]GTTGGTTTC CTGAAGTCCTAT TTGA	C	T		SILENT-NONCODING	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1823	cg42714160	874	GAGGAGGAAGA AAAACAGGCCGA GT[G/gap]AAGGT GCTGGAAAGGG AGGGAGGAC	G	gap		SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEOBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-123	
1824	cg43983244	2635	AGGAGAGGAAG GCCAAAAAAAAA AA[gap/A]TTGGA AAAGAGGGCGG GGGACCCCT	gap	A		SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P43271 PAIRED MESODERM HOMEOBOX PROTEIN 1 (HOMEOBOX PROTEIN MHOX) (HOMEOBOX PROTEIN K-2) (RHOX) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 217 aa.	2.20E-113	
1825	cg43917865	274	AGGCGCGCGCG GGAGGGTCCGC CCG[G/gap]CCAG GGCCCCGGGCG CTCGCAGAGG	G	gap		SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P28360 HOMEOBOX PROTEIN MSX-1 (HOX-7) - HOMO SAPIENS (HUMAN), 297 aa.	1.10E-111	4 (4p16.1)
1826	cg42714192	94	TATTATCATCATC ATCATCATCATC[A/gap]TCATCGAA GTATTTCACGTC CAGAG	A	gap		SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEOBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-108	
1827	cg43988025	1278	TTCTGAGAACTG ACTAGAGAAGAC A[G/A]AAAAATAG CCCGATGTAGGT TTCGG	G	A		SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEOBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17
1828	cg43988025	1279	TCTGAGAACTGA CTAGAGAAGACA G[A/G]AAAATAGC CCGATGTAGGTT TCGGT	A	G		SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEOBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17

1829	cg43988025	1320	GGTTTCGGTGTCCCCATATAGGCCC[gap/C]GTCCACACAGGCTTGACTGGGTGGA	gap	C			SILENT-NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEOBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17
1830	cg43268289	1110	TTCTTCCCTCTCTCCCTTTCTCCTC[T/C]CCCTGCTTTCTTGAAAAGGACTGAA	T	C			SILENT-NONCODING	homeobox	Human Gene Similar to SWISSPROT-ID:Q92988 HOMEOBOX PROTEIN DLX-4 (DLX-7) (DLX-8) - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.40E-90	17 (17q21.3)
1831	cg43268289	1218	TGTATGCCTTTGGCCTTGCACAACC[C/T]ATTTGTGAGCAAAAGCAGAAGTGGA	C	T			SILENT-NONCODING	homeobox	Human Gene Similar to SWISSPROT-ID:Q92988 HOMEOBOX PROTEIN DLX-4 (DLX-7) (DLX-8) - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.40E-90	17 (17q21.3)
1832	cg43988195	2818	TTTTTTTGGCTTTTAGTCCAGAAGG[A/gap]CCTCATCTCTGCACCTCTTACTTGA	A	gap			SILENT-NONCODING	homeobox	Human Gene Similar to SPTREMBL-ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1833	cg43988195	2902	GGAATAAGAGGATGTGGGGCACTGC[C/gap]AAGGGCAAGGTCAAAAATCAGGGTT	C	gap			SILENT-NONCODING	homeobox	Human Gene Similar to SPTREMBL-ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1834	cg43988195	333	GAAGATGAATACACAGAGTCTTTTG[T/A]TTCTCTATCAAATGTGGTTTTTTTA	T	A			SILENT-NONCODING	homeobox	Human Gene Similar to SPTREMBL-ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1835	cg43988195	334	AAGATGAATACACAGAGTCTTTTGT[T/A]TCTCTATCAAATGTGGTTTTTTTAT	T	A			SILENT-NONCODING	homeobox	Human Gene Similar to SPTREMBL-ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12

1836	cg43988195	744	ATGAAGAGAAAA TCCACCTAGCTC A[A/T]GGGGGCA GTGAAGATGAGG AAAGAA	A	T			SILENT-NONCODING	homeobox	Human Gene Similar to SPTREMBL-ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1837	cg43922794	199	GGGGAAGCAGC ATTTGCAGCCGG AG[gap/G]ATCGC GGAGTCCCAATG AACGGGC	gap	G			SILENT-NONCODING	hydrolase	Human Gene SWISSPROT-ID:Q14694 PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0190) - HOMO SAPIENS (HUMAN), 798 aa.	0.00E+00	14
1838	cg43296921	110	GCACAATGGCTT TATTTGTCACTG A[A/G]TGGCGGA CCAGGCCTACAG CCCGAG	A	G			SILENT-NONCODING	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)
1839	cg43296921	153	AGCCCGAGGGA GGACCCCAGTCA CA[G/gap]GGTTG AAAGGGGTGCTT GAGCCCTT	G	gap			SILENT-NONCODING	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)
1840	cg43296921	180	GTTGAAAGGGGT GCTTGAGCCCTT T[G/T]TTTCCAGA AGAGCAGAGAAA ATCTC	G	T			SILENT-NONCODING	hydrolase	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)

1841	cg43927025	2499	TATAATTACTTTA GCTGCACTAACA [G/gap]TACAATG CTTGTTAATGGT TAATAT	G	gap			SILENT-NONCODING	hydrolase	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.10E-224	10 (10q24)
1842	cg43923662	111	GATTTCATCAAC ATACAAGCCAAA C[A/G]AAGATCCC ATTTCAATTAGAT ATAC	A	G			SILENT-NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1843	cg43923662	153	TAGATATACCAC TCAAGAGAATCT C[C/T]AAAGATCT TCACATTTTTCCA TCTT	C	T			SILENT-NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1844	cg43923662	366	ATTCTGATAATTT TCACGTCATGAA[A/T]TATTAGTCTT TGATTTCTTTTCC CA	A	T			SILENT-NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1845	cg43305744	955	GGAAGCTGTGGT CCGATAAAGCCT G[G/gap]CGCAGC CTGTTTGTTGGT GACAACC	G	gap			SILENT-NONCODING	hydrolase	Human Gene Similar to SWISSPROT-ID:Q61068 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1) - MUS MUSCULUS (MOUSE), 526 aa.	1.10E-61	

1846	cg43951711	737	TATAATCAAAGG TACTATTATTGAT [C/T]ACAATTTAT TTTAAAGTCAGG AAAA	C	T			SILENT-NONCODING	hydrolase	Human Gene Similar to SWISSPROT-ID:Q92353 PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 467 aa.	5.00E-58	18
1847	cg43969804	166	CCACTTTCCCTG GGGTATTGCTTT G[C/gap]CCCTGT GCCTCCCACCCC AGGAAGC	C	gap			SILENT-NONCODING	hydrolase	Human Gene Similar to SWISSPROT-ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1848	cg43969804	307	TTCCCCAGGGAC AACCATCCTCTC C[C/gap]TGTGTC CCCTGCCCCCCA CACTGAG	C	gap			SILENT-NONCODING	hydrolase	Human Gene Similar to SWISSPROT-ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1849	cg43969804	53	GTTTAATGGGAC CATCACCGTGAT A[C/G]CCCATCAC AGCAGTCCCAG GCTGGA	C	G			SILENT-NONCODING	hydrolase	Human Gene Similar to SWISSPROT-ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1850	cg43929210	169	CTAAGGAAACAG GACTTGGGCAAA A[gap/T]TTTTTTA TTATGAAGATAC AGATCT	gap	T			SILENT-NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA-DEHYDROGENASE 4 (EC 1.1.1.62) (17-BETA-HSD 4) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5

1851	cg43929210	175	AAACAGGACTTG GGCAAAATTTTT T[gap/T]ATTATGA AGATACAGATCT AAGAAC	gap	T		SILENT-NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA-DEHYDROGENASE 4 (EC 1.1.1.62) (17-BETA-HSD 4) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5
1852	cg43998672	1777	CGGCCAAGGCC AGCGCTCCATGG CG[G/gap]CCCAG CGGGCTGGGGC GGGGCGGGG	G	gap		SILENT-NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1853	cg43998672	281	CAGTGAAGTCTT GCATGAGACTCC C[C/gap]ATCCAG CGGAGTTCTCCA AGCTGCA	C	gap		SILENT-NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1854	cg43998672	384	CGCAGAGGCTC ACTGGGAAACCT TG[G/gap]CCTCA CCGGGCCTGGA TTGGGCATC	G	gap		SILENT-NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1855	cg43998672	553	AGTGGCTGGGC CATAGGTGCACA TG[G/gap]CTCAC CGAGCCACTGCT GGGGAAGG	G	gap		SILENT-NONCODING	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
1856	cg42886248	195	TTAATATAACTAT CTGGTAATTATA[C/T]CTATGTTTAC TAACAATTTTACA AC	C	T		SILENT-NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P28845 CORTICOSTEROID 11-BETA-DEHYDROGENASE, ISOZYME 1 (EC 1.1.1.146) (11-DH) (11-BETA-HYDROXYSTEROID DEHYDROGENASE 1) (11-BETA-HSD1) - HOMO SAPIENS (HUMAN), 292 aa.	8.50E-151	1

1857	cg43955809	938	TTCCCCCCCGCT TTTTTTTTTTTT[T/gap]TGACTTTG CCTTGGAGAGCC AGAGC	T	gap			SILENT-NONCODING	immunoglob	Human Gene Similar to SWISSPROT-ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.90E-72	4
1858	cg43955809	939	TCCCCCCCGCTT TTTTTTTTTTT[T/gap]GACTTTGC CTTGGAGAGCCA GAGCT	T	gap			SILENT-NONCODING	immunoglob	Human Gene Similar to SWISSPROT-ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.90E-72	4
1859	cg43955809	697	GATGTAAAACCA ACTCCCCGCCCC C[C/A]AAAAAATT AAAATAGTCACA TTGGT	C	A			SILENT-NONCODING	immunoglob	Human Gene Similar to SWISSPROT-ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.9E-72	4
1860	cg43955809	892	AACTCAAGGAGT GAAAATCAGGAG G[G/T]GTAATAAA ATGTTCCTCGCA TTCCC	G	T			SILENT-NONCODING	immunoglob	Human Gene Similar to SWISSPROT-ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.9E-72	4
1861	cg41382080	146	ACACAATCATTG ACTATTAGAGGC C[A/C]GAGGAGA ATGAGGCCTGG CCTGGGA	A	C			SILENT-NONCODING	immunoglob_recept	Human Gene Similar to SWISSPROT-ID:P08118 PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA-MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PN44) HOMO SAPIENS (HUMAN), 114 aa.	2.6E-60	10 (10q11.2)

1862	cg41382080	179	ATGAGGCCTGG CCTGGGAGCCC TGT[G/A]CCTACT AGAAGCACATTA GATTATC	G	A			SILENT-NONCODING	immunogl ob_recept	Human Gene Similar to SWISSPROT-ID:P08118 PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA-MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PN44) HOMO SAPIENS (HUMAN), 114 aa.	2.6E-60	10 (10q11.2)
1863	cg43925670	155	ATTAAAAAAGCA CTCCCAATACCC C[gap/C]ATTCCA TAGGATTAACAG CTAGTAT	gap	C			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.|pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
1864	cg43925670	241	CCAGGTATATGT ACATTTTTTTAGG [C/G]ACTTAGACC TTATCTCCATAAA CAT	C	G			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.|pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1

1865	cg43925670	73	AAAGATAATGTTTATTTATTTTTTC[A/T]AATTATAGAAGTTGTAGATGCAAAA	A	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.|pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
1866	cg43925670	74	AAGATAATGTTTATTTATTTTTTCA[A/T]ATTATAGAAGTTGTAGATGCAAAAT	A	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.|pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
1867	cg42701070	216	AACCATGGGAAGCAGGGGGCATGGC[C/gap]ACTGGATCTGAAAGGGACCGGCTAA	C	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P20592 INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXB (P78-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 715 aa.	0	21
1868	cg43933380	148	TTTTAAGTCCAATTTTGAAAAGCTT[G/C]CAGAATTTCTTCTGAAATTACTTAA	G	C			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6

1869	cg43933380	149	TTTAAGTCCAATTTTGAAAAGCTTG[C/G]AGAATTTCTTCTGAAATTACTTAAA	C	G			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1870	cg43933380	1521	CCGTTCATTCTCACATACACATTGT[T/gap]ACACCCTAATGTAACAGGTAGTTTC	T	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1871	cg43933380	200	TTACTGTATGCATAAACTTACAAAA[gap/C]ACATATGCTATACCAAGGCAGAGAA	gap	C			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1872	cg43933380	228	ATATGCTATACCAAGGCAGAGAAAA[G/A]AAAAAAAGTGAAGTGGCTACAAAGG	G	A			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1873	cg42489246	610	GTTGCAGTGAGCCAAGATCGTGCCA[C/T]TCCACTCCAGCCTGGGTGATAGGTG	C	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P48551 INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	1.7E-256	21 (21q22.1)
1874	cg43931810	552	CACACCATGAGGAGCGAGGGCTCAG[C/G]TCTCCCCAGGGCCCTGGAAATCCAT	C	G			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q14653 INTERFERON REGULATORY FACTOR 3 (IRF-3) - HOMO SAPIENS (HUMAN), 427 aa.	1.2E-240	19

1875	cg43956260	210	ATGAAAGAGGGCT GTATATCTCAAA A[T/A]TAAAAAAA AAAAAAGGATAA AAAAT	T	A		SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1876	cg43956260	224	ATATCTCAAAATT AAAAAAAAAAA[A/gap]GGATAAAA AATTAGCCTTGA GTTCT	A	gap		SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1877	cg43956260	51	TTTTTTTTTTTT TTCCTCTTTCAA[T/A]AAAATTTTAT TTTAAGTCCTTA GTG	T	A		SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1878	cg43956260	89	TAAGTCCTTAGT GAATATCTAAGA G[G/A]AAAATATA AAGTGCTTGGCT TTAGA	G	A		SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14

1879	cg43082514	1381	TGATTGCTGTGTCCAACTCCAGTAC[gap/C]TGGAGCTTCTCTTTAACTCAGGACT	gap	C			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.5E-188	4 (4q35.1)
1880	cg43082514	2153	GTTGTTATTACATCCTTGTGGCACA[T/gap]TTTTTTTTTAATTTTGTAAAGGTG	T	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1881	cg43082514	2162	ACATCCTTGTGGCACATTTTTTTTT[T/gap]TAATTTTGTAAAGGTGAAAAAAGCT	T	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1882	cg43082514	2163	CATCCTTGTGGCACATTTTTTTTTT[T/gap]AATTTTGTAAAGGTGAAAAAAGCTT	T	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1883	cg43082514	2163	ATCCTTGTGGCACATTTTTTTTTT[gap/T]AATTTTGTAAAGGTGAAAAAAGCTT	gap	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1884	cg43082514	2201	GTGAAAAAAGCTTTTATGAGCTCAT[G/C]TAGCAATCAGATTTTCCTGTGGATT	G	C			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1885	cg43983653	135	CAAATGTACATATTTACACACGTCC[gap/T]TATGTGTTCACACATGACTTAATGG	gap	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)

1886	cg43983653	136	AAATGTACATATT TACACACGTCCT[gap/T]ATGTGTTC ACACATGACTTA ATGGT	gap	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1887	cg43983653	2064	GAGGTTGCCGG GTTCTTAAGGCA GC[C/gap]GGGCA CGGCCGGCGTG GACTGGGCA	C	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1888	cg43983653	261	GGCTTGAGGGG GTGGTGGGCGC CGA[G/gap]CAAG GCACTGTATAAA TAAATGCAA	G	gap			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1889	cg43983653	432	AGCTCCTCTGAG GCTGAGGGAGC AT[C/T]GCCCCGA AGGACCCCACTT TCCTTC	C	T			SILENT-NONCODING	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1890	cg42918267	59	TAAGCTAAAAAC AAAATCAACCGG G[A/T]CCCCAGCT TTTCAGAACTGC AGGGA	A	T			SILENT-NONCODING	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	
1891	cg42918267	72	AAATCAACCGGG ACCCCAGCTTTT C[A/G]GAACTGC AGGGAAACAGC CATCATG	A	G			SILENT-NONCODING	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	
1892	cg42918267	82	GGACCCCAGCTT TTCAGAACTGCA G[G/A]GAACAG CCATCATGAGTG AGGTCA	G	A			SILENT-NONCODING	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	

1893	cg3000751	184	TCACCCATCTCAGCAAGCCCAGAAG[T/C]ATCTGCAATATCTACGATGGCCTCG	T	C			SILENT-NONCODING	interferon	Human Gene Similar to SWISSPROT-ID:P01562 INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D) - HOMO SAPIENS (HUMAN), 189 aa.	8.20E-98	9
1894	cg3000751	199	AGCCCAGAAGTATCTGCAATATCTA[C/T]GATGGCCTCGCCCTTTGCTTTACTG	C	T			SILENT-NONCODING	interferon	Human Gene Similar to SWISSPROT-ID:P01562 INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D) - HOMO SAPIENS (HUMAN), 189 aa.	8.20E-98	9
1895	cg43510640	187	GATAGAGTACGTGGGATACAGGTCA[C/T]GGGCAGACTCCTGGCCTCAATGATG	C	T			SILENT-NONCODING	interferon	Human Gene Similar to SWISSPROT-ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1896	cg43510640	227	CCTCAATGATGCCTCCTGATCTATC[G/C]CTAGGCCTGGACGACCAACACTGGG	G	C			SILENT-NONCODING	interferon	Human Gene Similar to SWISSPROT-ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1897	cg44339782	187	GATAGAGTACGTGGGATACAGGTCA[C/T]GGGCAGACTCCTGGCCTCAATGATG	C	T			SILENT-NONCODING	interferon	Human Gene Similar to SWISSPROT-ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1898	cg44339782	227	CCTCAATGATGCCTCCTGATCTATC[G/C]CTAGGCCTGGACGACCAACACTGGG	G	C			SILENT-NONCODING	interferon	Human Gene Similar to SWISSPROT-ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1899	cg43978774	16	TTTTTTTTTTTTTT[C/T]TCTCATTTAAAAATATTTATTGAGC	C	T			SILENT-NONCODING	interferon	Human Gene Similar to SWISSNEW-ID:Q99873 PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-) (INTERFERON RECEPTOR 1-BOUND PROTEIN 4) - HOMO SAPIENS (HUMAN), 361 aa.	3.50E-50	3

1900	cg43922672	2259	CACCCAGCAAAAGGTTGTTCCTAAA[A/G]TAAGGGCAGAGTCACACGGGGGCAG	A	G			SILENT-NONCODING	interleukin	Human Gene TREMBLNEW-ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0.00E+00	15
1901	cg43922672	2277	TCCTAAAATAAGGGCAGAGTCACAC[G/T]GGGGCAGCTGATACAAATTGCAGAC	G	T			SILENT-NONCODING	interleukin	Human Gene TREMBLNEW-ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0.00E+00	15
1902	cg42271251	256	TTGTTCAAGAGTTCCCTATCACTCT[C/gap]TTTAATCACTACTCACAGTAACCTC	C	gap			SILENT-NONCODING	interleukin	Human Gene Homologous to SPTREMBL-ID:Q14629 INTERLEUKIN 2/BCM FUSION PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	9.60E-120	4 (4q26)
1903	cg42908571	1039	TTTATGTAAGTCATATTTATATTTT[T/gap]AAGAAGTACCACTTGAAACATTTTA	T	gap			SILENT-NONCODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
1904	cg42908571	155	CTGAGGCTCATTCTGCCCTCGAGCC[C/gap]ACCGGGAACGAAAGAGAAGCTCTAT	C	gap			SILENT-NONCODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
1905	cg42887911	900	ACAGTCCTTCCGTGAGGCCTGGGGG[G/A]CATCTGTGCCTTATTTATACTTATT	G	A			SILENT-NONCODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P20809 INTERLEUKIN-11 PRECURSOR (IL-11) (ADIPOGENESIS INHIBITORY FACTOR) (AGIF) - HOMO SAPIENS (HUMAN), 199 aa.	2.50E-103	19

1906	cg43994858	323	CAGCAAATTGTCCCTGCTTTAGTCA[C/T]AGCAATTTTTCATGTCCTCTGTTGC	C	T			SILENT-NONCODING	interleukinrecept	Human Gene SWISSPROT-ID:P24394 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN PRECURSOR (IL-4R-ALPHA) (CD124 ANTIGEN) - HOMO SAPIENS (HUMAN), 825 aa.	0.00E+00	16 (16p12.1)
1907	cg43987278	710	GAGTTGATCTGATTGGCTAGTTCAG[G/gap]CCCAGCCTACCTGATTGGACAGAGC	G	gap			SILENT-NONCODING	interleukinrecept	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1908	cg43987278	98	ACAGAGTAACAAAGATTTTTCTTTA[A/gap]ATAAATGTATTTCAACGAAAATGAA	A	gap			SILENT-NONCODING	interleukinrecept	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1909	cg43987278	99	CAGAGTAACAAAGATTTTTCTTTAA[A/gap]TAAATGTATTTCAACGAAAATGAAC	A	gap			SILENT-NONCODING	interleukinrecept	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1910	cg43091826	1583	CTTCTAACCACCCTGTCTCCAGCTG[C/gap]TCTGCACACATGGACAGGGACCTGG	C	gap			SILENT-NONCODING	interleukinrecept	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN-15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)
1911	cg43091826	1621	GACAGGGACCTGGGAAAGGTGGGAG[A/G]GATGCTGAGCCCAGCGAATCCTCTC	A	G			SILENT-NONCODING	interleukinrecept	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN-15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)

1912	cg43091826	265	CCTGGGCAGCG CTCGCCCGGGG AGT[G/C]CAGCG GTGTCCTGTGGA GCTGCCGC	G	C			SILENT-NONCODING	interleukinrecept	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN-15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)
1913	cg43926168	40	ATTCCGGTTTTTT TTTTTTTTTTT[A /T]GGCATTTTCA AGATTTTATTGTA AA	A	T			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.80E-94	2 (2q14.2)
1914	cg43278750	1578	AGTTCTCTAAAT GTTGCTTTTCTC A[G/A]CCTGTTTA TCCATATTTCAAT CCTT	G	A			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1915	cg43278750	1583	TCTAAATGTTGC TTTTCTCAGCCT G[T/C]TTATCCAT ATTTCAATCCTT GGAAC	T	C			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1916	cg43278750	1611	ATCCATATTTCAA TCCTTGGAACTG[T/C]CCAGCTCCC ATGACTCTATGC CCAC	T	C			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1917	cg43278750	1613	CCATATTTCAAT CCTTGGAACTGT C[C/T]AGCTCCCA TGACTCTATGCC CACCA	C	T			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1918	cg43278750	1616	TATTTCAATCCTT GGAACTGTCCAG [C/T]TCCCATGAC TCTATGCCCACC AAGC	C	T			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	

1919	cg43278750	1617	ATTTCAATCCTTGGAACTGTCCAGC[T/C]CCCATGACTCTATGCCCACCAAGCT	T	C			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1920	cg43278750	1627	TTGGAACTGTCCAGCTCCCATGACT[C/G]TATGCCCACCAAGCTCTTGAATTTT	C	G			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1921	cg43278750	1650	CTCTATGCCCACCAAGCTCTTGAAT[T/G]TTCTCATTTCTTCACCTACAACCCT	T	G			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1922	cg41657511	1553	TTGAGCATTTTTTTTTTAGGATGGG[A/gap]GGTGCGTGAGGTTCTCTCAGCCCAG	A	gap			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1923	cg41657511	1560	TTTTTTTTTAGGATGGGAGGTGCG[T/A]GAGGTTCTCTCAGCCCAGGGGGGTG	T	A			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1924	cg41657511	1561	TTTTTTTTAGGATGGGAGGTGCGT[G/T]AGGTTCTCTCAGCCCAGGGGGGTGC	G	T			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11

1925	cg41657511	1618	GTAAGGACAGCCTTCACTGTGCCTT[C/T]GAGCTGCTTTCCGCTCCCTGGGCTC	C	T			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1926	cg41657511	1698	TGGCAGGGATGTTCTAGAAATGGGG[G/gap]TTGGTTCCTCTAGCTACCCCAAATG	G	gap			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1927	cg43929155	1432	AACTGAACATTCCAGAGCGTGTAGT[G/T]AATCACGTAAAGCTAGAAATGATCC	G	T			SILENT-NONCODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P21109 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1) - ORYCTOLAGUS CUNICULUS (RABBIT), 355 aa.	4.20E-55	2
1928	cg43933187	44	TTTTTTTTTTTTTTTTTTTTTT[G/T]CAATGTTTAGAACATTTTATTAAAG	G	T			SILENT-NONCODING	isomerase	Human Gene SWISSNEW-ID:P11388 DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1531 aa.	0.00E+00	17 (17q21)
1929	cg43933187	458	TAGACACAGCCAAAGTGTTTTTCTT[C/T]GGCCTCTGATGATTTGAGAAGATGA	C	T			SILENT-NONCODING	isomerase	Human Gene SWISSNEW-ID:P11388 DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1531 aa.	0.00E+00	17 (17q21)
1930	cg43951261	5307	CTTGTAGAATTGTTATAGACTGCCG[T/gap]GCATTAGCACAGATTTTAATTGTCA	T	gap			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0.00E+00	3 (3p)

1931	cg40915009	3857	GACCAGCCAGG GCAACATGGTGA AA[A/gap]CCCCA TCTCTACTAAAA AACAAAAA	A	gap			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1932	cg40915009	3875	GGTGAAAACCCC ATCTCTACTAAA A[A/T]ACAAAAAA TTAGCCAGGTGT GGCGG	A	T			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1933	cg40915009	3944	GCTACTTAGGAG GCTGAGGCAGG AG[A/G]ATCACCT GAACACAGGAG GTAGAGG	A	G			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1934	cg40915009	3950	TAGGAGGCTGA GGCAGGAGAAT CAC[C/T]TGAACA CAGGAGGTAGA GGCTGCAG	C	T			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1935	cg40915009	3954	AGGCTGAGGCA GGAGAATCACCT GA[A/G]CACAGG AGGTAGAGGCT GCAGTGAG	A	G			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0	
1936	cg40915009	3958	TGAGGCAGGAG AATCACCTGAAC AC[A/G]GGAGGT AGAGGCTGCAGT GAGCCGT	A	G			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0	
1937	cg43993971	78	TTTTTACCTCCTC CGTGGCATCTTT[A/G]TTTTTCTACA TGGGATGTGAAC AAC	A	G			SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:P06744 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) (NEUROLEUKIN) (NLK) - HOMO SAPIENS (HUMAN), 558 aa.	3.6E-305	19 (19q13.1)

1938	cg43930054	587	TGGCTGGCAGA GGAGAGCTGGG GAG[G/gap]CTGC AGCCTTTACAGC AGACAGCAG	G	gap		SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
1939	cg43969064	561	AGAAACACATTA GGGATCATATTC A[T/C]AGACAAAA ACCTTTACATTTT CTTA	T	C		SILENT-NONCODING	isomerase	Human Gene SWISSPROT-ID:Q08752 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 370 aa.	1.3E-200	4
1940	cg44001328	215	TGTGGAAGATAA GAGTTAGAGACC T[C/A]GGCCTCCT GGTCAGTGGAG CCCTTG	C	A		SILENT-NONCODING	isomeras e	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.|pdb:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1941	cg44001328	237	CCTCGGCCTCCT GGTCAGTGGAG CC[C/gap]TTGGC CTCATGCCTGGT GGGCTAAG	C	gap		SILENT-NONCODING	isomeras e	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.|pdb:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1942	cg44001328	308	GGTAGGGGAGG CCTTGGCTTGGC CC[C/gap]AGCAG CTCCAGGGCCCT GAGTTCCT	C	gap		SILENT-NONCODING	isomeras e	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.|pdb:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1

2518	cg43139469	402	GCTCAGGGTTTC TGCAGTGTCTTT T[gap/T]GGTGAC TTGTTAGCAGCC AGTGGCT	gap	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7.00E-259	5 (5q31)
2519	cg43980696	528	CCCCCCAGTGAA AGCTGGGCTGG GC[A/T]GGGAGT CCTCAGAAGCCA CTCTGGC	A	T			SILENT-NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q28647 PROTEIN PHOSPHATASE 2A0 B' REGULATORY SUBUNIT ALPHA ISOFORM - ORYCTOLAGUS CUNICULUS (RABBIT), 500 aa.	9.10E-250	11
2520	cg43918944	2303	TGAATGAATTTTA TCATCTATGATA[T/A]GAGTGAGAT AATTATGGGAGT GGTA	T	A			SILENT-NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
2521	cg43918944	2374	TCTTTGATTGTG TTGCACATAGAT A[T/C]GGTAGTCT GCTCTGTATATT TTTCC	T	C			SILENT-NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
2522	cg43336281	99	CTTTCTGGCATC TTGGGACTTGTC C[C/gap]TAAGAA TAGGGAAGACAG TCATCCT	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2523	cg43336281	131	TAGGGAAGACAG TCATCCTGTCCT G[G/gap]AGCAAA GCTCCCCCTTGC ACAGGAA	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2524	cg43336281	141	AGTCATCCTGTC CTGGAGCAAAGC T[C/gap]CCCCTT GCACAGGAACAC AACTCCC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22

2525	cg4336281	1631	AGCGACTATGTTTAAGGTTTTTTTT[T/gap]GTAAATAAGAGACCTTAAGCAATGC	T	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2526	cg4336281	2528	AGAGCCCCGCTGTCGGGCCCAGGCA[C/A]CACTACGTGGCAGTCGCAGCTCCTG	C	A			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2527	cg4336281	299	AGAATGCACAGGACTCTGGGGGCTG[C/gap]CCCCCTTGAGCTACAGAGGCAGAAT	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2528	cg4336281	326	CCCCTTGAGCTACAGAGGCAGAATC[G/A]AACCAAAAACACTGCTTCCTTTAAC	G	A			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2529	cg4336281	394	CATTTAGCTTGGGACGAGGCTAGGC[C/gap]TAAGAAGGGCCAGAGCTGTCCTCCC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2530	cg4336281	830	ATCTCCCCAGGACACGCCGGCTCAC[C/T]TGCACCCACAGCGTTCTAGGAGGTC	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2531	cg4336281	97	GCCTTTCTGGCATCTTGGGACTTGT[C/gap]CCTAAGAATAGGGAAGACAGTCATC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22

2532	cg43988504	2416	CAGTTTTCCAGGAATAGGCATTTGC[C/gap]TAATTCCTGGCATGACACTCTAGTG	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.|pcls:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2533	cg43988504	3028	CCAGGCTGTAAGCATTCTGAGCTGG[G/gap]CTTGTTGTTTTTAAGTCCTGTATAT	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.|pcls:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2534	cg43988504	60	GGCCTCGGGGCTAAGAGCGCGACGC[G/gap]GCCTAGAGCGGCAGACGGCGCAGTG	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.|pcls:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2535	cg43988504	61	GCCTCGGGGCTAAGAGCGCGACGCG[G/gap]CCTAGAGCGGCAGACGGCGCAGTGG	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.|pcls:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2536	cg43983327	1820	CAGCCAGCCACATTTCCCTGTGTCT[G/gap]GCTAGAGCCACCATTAGACTCAGAC	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11117 LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) - HOMO SAPIENS (HUMAN), 423 aa.	1.90E-233	11 (11p12)

2537	cg43983327	1821	AGCCAGCCACATTTCCCTGTGTCTG[G/gap]CTAGAGCCACCATTAGACTCAGACA	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11117 LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) - HOMO SAPIENS (HUMAN), 423 aa.	1.90E-233	11 (11p12)
2538	cg44004203	103	AATATAGAATCCCACTAGCAGCTTT[G/gap]CTTAGTGATCAAGACGTTTTTGGGA	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2539	cg44004203	1659	TACTAAATGTGATCTAAGAGAATAT[G/C]GTTCCACCCAGTGTGGAGCCATGAA	G	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2540	cg44004203	1660	ACTAAATGTGATCTAAGAGAATATG[G/C]TTCCACCCAGTGTGGAGCCATGAAA	G	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2541	cg44004203	1728	ACATAAAGATGCCATTGTAGTAGAA[A/gap]TGCACAAATGCATGTAATAACTGCA	A	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2542	cg44004203	1827	ACTCAGACTTCGTTCAAAGTGACAG[gap/G]AACGAGGGGAGTGGAGTGCAAAGGA	gap	G			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	

2543	cg44004203	2018	GGGTAGGAGGGCAACAAACACATCC[C/T]TAGGTGAAGGAGTGTAAATACAGAT	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2544	cg44004203	659	CCTCTTTTTGTGATCACTTTCTGGC[C/gap]TTGCGGAGATGACAAACCTGTTCTG	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2545	cg43984194	249	TAGCCCCAAGATTGAGATTCTTATG[gap/G]AATACACTGTATTATTACCTGCAAT	gap	G			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P35813 PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) - HOMO SAPIENS (HUMAN), 382 aa.	1.9E-208	14
2546	cg43984194	252	GCCCCAAGATTGAGATTCTTATGAA[T/C]ACACTGTATTATTACCTGCAATACT	T	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P35813 PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) - HOMO SAPIENS (HUMAN), 382 aa.	1.9E-208	14
2547	cg43307343	460	AAAATTTATAGCTGCAGAATATTCT[C/T]AAGTCATGAATATTAGGTGTCTGTC	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P17706 T-CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	3.6E-207	18 (18p11.3)
2548	cg43969460	167	CCTGGACTCGGAGGAAGGCCGAGAG[G/gap]ACACGGACGGTGGCCACACCACGCT	G	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	

2549	cg43969460	187	GAGAGGACACG GACGGTGGCCA CAC[C/gap]ACGC TGCAGTGAAGGC CCAAGTGTG	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	
2550	cg43969460	215	GCTGCAGTGAAG GCCCAAGTGTGA T[G/C]GCAGAGA AAGAGGGAAAGT TGGAGA	G	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	
2551	cg43933809	1541	CATTTAGTCTTTA AAAAAAAAAAAA[gap/A]GGATTCCT ATTAACCAACAT ACTTA	gap	A			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE)., 327 aa.	1.6E-181	2 (2p23)
2552	cg43933809	2090	GCAGTAAGTAAT ACAATGTGCCAA T[C/T]CATAAAAT GTAAGTTAACAG GTTTC	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE)., 327 aa.	1.6E-181	2 (2p23)
2553	cg43933809	2378	TTGTTAATACTAA CCCTTAAAAAAA[A/gap]GAAATAGG AAAAGAAAGGCT GCAAT	A	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE)., 327 aa.	1.6E-181	2 (2p23)

2554	cg43933809	3189	AATAGTTGGTGAATGTCTGTAAAGC[T/C]CTTCCCATATTTCACTTTTAAAAAT	T	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE)., 327 aa.	1.6E-181	2 (2p23)
2555	cg43933809	3190	ATAGTTGGTGAATGTCTGTAAAGCT[C/T]TTCCCATATTTCACTTTTAAAAATG	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE)., 327 aa.	1.6E-181	2 (2p23)
2556	cg43917813	1566	TGAAATTTAGTACACTATGTTCTAG[gap/G]GTCAGTCTAACAGTTTGCCTGCTGT	gap —	G			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11082 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 309 aa.	5.3E-174	8
2557	cg43917813	1892	TAAATTACTGTTTTATGTTGATCTG[C/T]ATATTTCTGTATATTTGTCATGACA	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11082 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 309 aa.	5.3E-174	8
2558	cg43269274	15	TTTTTTTTTTTTT[C/T]TCCTTTTACTATTTTTATTTTACAC	C	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10

2559	cg43269274	164	AACTAACAGACA AAAAGAAAAAAA A[A/gap]GTAGTA CCACGTTGCAAA ATCTGCA	A	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2560	cg43269274	208	ATCTGCAAATCC CAGAAGTCCACA G[C/gap]TTGAAG ACAACCTCCAGG GGCAGGG	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2561	cg43269274	22	TTTTTTTTTTTTT TCTCCTTT[T/C]A CTATTTTTATTTT ACACTATAAAA	T	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2562	cg43269274	40	CTCCTTTTACTAT TTTTATTTTACA[C/gap]TATAAAAA ACAAGAACAACA ACAAC	C	gap			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2563	cg43269274	53	TTTTATTTTACAC TATAAAAAACAA[G/C]AACAACAAC AACAACCAGTAA CATA	G	C			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2564	cg43269274	635	CATGTCCCTACA AACCCTGTAGGG T[G/T]ACTTTCCC AACTAGACGGTG ATCAG	G	T			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10

2565	cg43269274	816	CCCACGTTGCTG CAGGTATTTATT G[C/G]CTTATGCT TGAAATGAAAAG GCGAA	C	G			SILENT-NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2566	cg43972150	119	AACAGCCAGCCA TGGCCTGCTGGA A[G/gap]CCAGGG GACAATTCTTCA TACACAG	G	gap			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2567	cg43972150	299	CATGGCGGAGG CAAGTGCTGGAT GT[G/gap]GGGAC AGGCCATGTCCC CAAAGCCC	G	gap			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2568	cg43972150	302	GCGGAGGCAAG TGCTGGATGTGG GG[gap/G]ACAGG CCATGTCCCCAA AGCCCCTA	gap	G			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2569	cg43972150	47	TTTTTTTTTTTT G]TAAAAGCCAC GCTAATAATTAC CCC	T	G			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2570	cg43972150	809	GAAATCCCAGAC CCTCTGCTCACT C[C/gap]TCACGG GGACAAGCTATG AGATGCC	C	gap			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17

2571	cg43967897	119	GCGCGGGAGGC GGTGGCGGCGG CTG[C/gap]CCGG GGCCAACATGAC CAGGCTCTG	C	gap			SILENT-NONCODING	phosphatase	Human Gene Similar to SWISSPROT-ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2572	cg43967897	121	GCGGGAGGCGG TGGCGGCGGCT GCC[C/gap]GGGG CCAACATGACCA GGCTCTGAA	C	gap			SILENT-NONCODING	phosphatase	Human Gene Similar to SWISSPROT-ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2573	cg43967897	197	GGACAGACTCG CTGCGGCTCCG GAG[G/gap]CAGT GATTCCAAGCTG CTCGCGCAC	G	gap			SILENT-NONCODING	phosphatase	Human Gene Similar to SWISSPROT-ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2574	cg43967897	234	AGCTGCTCGCG CACGCTGCTGCC AA[G/gap]CTGCA GGATGGTGCAC GTAGCCAGG	G	gap			SILENT-NONCODING	phosphatase	Human Gene Similar to SWISSPROT-ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2575	cg43272594	938	CCGGACCCCGC CCAGGCAGGGA GCT[G/A]CTGTGA GTCCAGCTGAG GCCCACCC	G	A			SILENT-NONCODING	phosphatase	Human Gene Similar to SPTREMBL-ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.4E-79	19

2576	cg43985274	912	CTTGGCTGGACC TGGAGGCCCTG CC[C/gap]AGCCC TGCTCTGCCCAG CCCAGCAG	C	gap			SILENT-NONCODING	phosphatase	Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa.|pcls:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa.|pcls:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70		
2577	cg43948077	1216	ACCCTTCCACCC CATTCCCACCCA A[T/G]CCCACCCT TCTCCATGACCA AAAAT	T	G			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1	
2578	cg43948077	342	TAGTCTTGGAGC TCTGAATAACAA G[A/G]GCTCTCAA TTGAGGGGGGA AAGAGC	A	G			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1	
2579	cg43948077	352	GCTCTGAATAAC AAGAGCTCTCAA T[T/G]GAGGGGG GAAAGAGCCTCC AAACTG	T	G			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1	
2580	cg43948077	359	ATAACAAGAGCT CTCAATTGAGGG G[G/T]GAAAGAG CCTCCAAACTGA CATCTA	G	T			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1	
2581	cg43948077	369	CTCTCAATTGAG GGGGGAAAGAG C[T/G]CCAAACT GACATCTAAAAA TTCCTC	T	G			SILENT-NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1	

2582	cg43948077	373	CAATTGAGGGG GGAAAGAGCCTC CA[A/T]ACTGACA TCTAAAAATTCCT CTTAG	A	T			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2583	cg43948077	376	TGAGGGGGGAA AGAGCCTCCAAA CT[gap/T]GACAT CTAAAAATTCCT CTTAGAGA	gap	T			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2584	cg43948077	381	GGGGGAAAGAG CCTCCAAACTGA CA[T/gap]CTAAAA ATTCCTCTTAGA GACACCA	T	gap			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2585	cg43948077	390	AGCCTCCAAACT GACATCTAAAAA T[T/C]CCTCTTAG AGACACCAGTTA CTTCC	T	C			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2586	cg43948077	393	CTCCAAACTGAC ATCTAAAAATTC C[T/C]CTTAGAGA CACCAGTTACTT CCAAA	T	C			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2587	cg43948077	413	ATTCCTCTTAGA GACACCAGTTAC T[T/gap]CCAAAC AAATCTTTTCCTT TTTAAT	T	gap			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2588	cg43948077	472	CCCAACTGGTCA TATCCTTTGAAA A[gap/A]CTGCCT TCATAATACACTT AAAAGT	gap	A			SILENT-NONCODING	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1

2589	cg43948077	488	CCTTTGAAACT GCCTTCATATA C[A/C]CTTAAAAG TAATGCCTTAGA GTAGA	A	C			SILENT-NONCODING	phosphataseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2590	cg43931444	1926	TTTGTAGCTGTT TAAAAAAAAAA A[A/gap]AAGGTA GCTGTGATACAA ACCCCAG	A	gap			SILENT-NONCODING	phosphataseinhib	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2591	cg43931444	1927	TTGTAGCTGTTT AAAAAAAAAAA A[A/gap]AGGTAG CTGTGATACAAA CCCCAGG	A	gap			SILENT-NONCODING	phosphataseinhib	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2592	cg43931444	1928	TGTAGCTGTTTA AAAAAAAAAAA A[A/gap]GGTAGC TGTGATACAAAC CCCAGGA	A	gap			SILENT-NONCODING	phosphataseinhib	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9

2593	cg43931444	612	CGCAGTAGACAGAGACAGACCGAGA[gap/G]AGGAAGGGAGAGACAGAGGGGGCGC	gap	G			SILENT-NONCODING	phosphataseinhib	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2594	cg43950308	662	TTATGTTACATCAAGGCAGCCATGC[C/gap]AATAAAATGGAAGGCTATGAAAGCA	C	gap			SILENT-NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P46019 PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) - HOMO SAPIENS (HUMAN), 1235 aa.	0	X (Xp22.2)
2595	cg43950308	806	AGGTGGCCCTTGTCAAGGCTACTGC[C/gap]GCCAGGAGGATCTTTGCATCTTTAG	C	gap			SILENT-NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P46019 PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) - HOMO SAPIENS (HUMAN), 1235 aa.	0	X (Xp22.2)
2596	cg43996195	357	GGCACGGGCTCCAGCTCTTGTGTAA[G/A]AAAGAACAGGAATGAGAACAGCTTT	G	A			SILENT-NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
2597	cg43947998	1288	AATAGGGGGAGAAGAGAATGGTGGG[G/T]TTTTTTTTCCCCCTTAAAATGTAAT	G	T			SILENT-NONCODING	phosphorylase	Human Gene SWISSPROT-ID:Q13126 5' METHYLTHIOADENOSINE PHOSPHORYLASE (EC 2.4.2.28) (MTA PHOSPHORYLASE) (MTAPASE) - HOMO SAPIENS (HUMAN), 283 aa.	2.8E-152	9 (9p21)

2598	cg43958858	2869	TTCTGTTTTGCTG TTTTTTTGTTTTG [gap/T]TTTTTTTTT CTCCAGAGCACT TTGGT	gap	T			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.|pcls:SWISSPROT-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)	
2599	cg43958858	2877	GCTGTTTTTTTTGT TTTGTTTTTTTTT[g ap/T]CTCCAGAG CACTTTGGTCTA GACTA	gap	T			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)	
2600	cg44016415	248	AGAAATGAGAAA AAAATAGCAAGC G[C/gap]CAGGGC CAATTAAGCATC CCTCTCC	C	gap			SILENT-NONCODING	polymerase	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2601	cg44016415	249	GAAATGAGAAAA AAATAGCAAGCG C[C/gap]AGGGCC AATTAAGCATCC CTCTCCC	C	gap			SILENT-NONCODING	polymerase	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X

2602	cg44016415	283	TTAAGCATCCCT CTCCCCGTTTTT C[T/gap]GAATAC AACACAGTGATC CTCACCG	T	gap			SILENT-NONCODING	polymerase	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2603	cg44016415	296	TCCCCGTTTTTC TGAATACAACAC A[G/gap]TGATCC TCACCGTAACCC CTACACA	G	gap			SILENT-NONCODING	polymerase	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2604	cg43282997	619	CGAGACAGGAG GCTGAACCCCG GAG[G/gap]CTGC AGCCAGGGAGG AGGCAGTGGG	G	gap			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P55199 RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) - HOMO SAPIENS (HUMAN), 621 aa.	5.5e-314	
2605	cg43282997	715	GGGAGGGCCGA GGTGGGCTTGC AGC[C/gap]ACCC GCCAGGGCCAG ACGTCTGCAG	C	gap			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P55199 RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) - HOMO SAPIENS (HUMAN), 621 aa.	5.5e-314	
2606	cg43993893	318	CAAAGGTTAAGA AATAAATTAAGA C[T/gap]CCTATT GGGTTGTGTCTG CCAGGGA	T	gap			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.|pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
2607	cg43993893	321	AGGTTAAGAAAT AAATTAAGACTC C[T/gap]ATTGGG TTGTGTCTGCCA GGGAGGA	T	gap			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.|pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)

2608	cg43993893	337	AAGACTCCTATTGGGTTGTGTCTGC[gap/G]CAGGGAGGATACAGGCCTCATTCGC	gap	G			SILENT-NONCODING	polymerase	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.|pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
2609	cg43935562	2098	CAGTCAGTTCATCCCTACCCTGGCC[C/T]AGATGATCACTGATCTTGTCATTAT	C	T			SILENT-NONCODING	polymerase	Human Gene TREMBLNEW-ID:G300898 A1 REPLICATIVE POLYMERASE ACCESSORY PROTEIN 38 KDA SUBUNIT - HOMO SAPIENS, 315 aa.	4.7E-166	13 (13q12.3)
2610	cg43939941	182	GACAATGATGGAGGCTCAGATCACA[C/T]TGCACCTCTTTAGTCTTCCAACTTG	C	T			SILENT-NONCODING	polymerase	Human Gene SPTREMBL-ID:Q19969 SIMILAR TO S. CEREVISIAE SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN - CAENORHABDITIS ELEGANS, 685 aa.	1.9E-160	13
2611	cg43916712	2631	GAGATTATGTTGTGCTCTTTATTGC[C/gap]AAAAATAAACACTTTTAAAAAGACA	C	gap			SILENT-NONCODING	polymerase	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
2612	cg43916712	3207	ACTAACCAGGAGAGAAGTCTAGTTG[G/gap]TTCCCTACAGGTGCACTGGAAACAC	G	gap			SILENT-NONCODING	polymerase	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
2613	cg43916712	4335	TTGGCGTACGGCATCTCGCCCAGGG[G/gap]CCACCAGCCTCCGCGTCTGCTCCGC	G	gap			SILENT-NONCODING	polymerase	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	

2614	cg43988515	577	AGAAACATTAAA CACTATGACACA T[G/T]ACCTTTTT AGCTATTTTTAAT AGTC	G	T			SILENT-NONCODING	polymerase	Human Gene Similar to SPTREMBL-ID:Q92811 RNA POLYMERASE II COMPLEX COMPONENT SRB7 - HOMO SAPIENS (HUMAN), 144 aa.	1.80E-70	12
2615	cg43935115	1077	TCCACAATACTT AGCACTTGTCCC C[gap/C]AAGTGT AAACACTTCCCA TGGCGTG	gap	C			SILENT-NONCODING	polymerase	Human Gene Similar to SWISSPROT-ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2616	cg43935115	1192	TAAGAATTTCAG GCCAGTTGTGGT G[G/gap]CTCATG CCTGTAATCTCA CCAGTTT	G	gap			SILENT-NONCODING	polymerase	Human Gene Similar to SWISSPROT-ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2617	cg43935115	1466	TCTCCATTTAAAA AAAAAAAAAAA[A/gap]GGCATTTC AAACTAACAGCG GTTTA	A	gap			SILENT-NONCODING	polymerase	Human Gene Similar to SWISSPROT-ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2618	cg43935115	314	GTTTTCCCCCAG ACTGAGATCAAG T[G/A]ACTTCACT GCAGTGGCTCAA GAGTG	G	A			SILENT-NONCODING	polymerase	Human Gene Similar to SWISSPROT-ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2619	cg43935115	810	GTAGCCTTGTCA TTGGGCACACAA C[A/C]ACCACAGT TCATACAGCAAA TGGGC	A	C			SILENT-NONCODING	polymerase	Human Gene Similar to SWISSPROT-ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2

2620	cg43948227	94	AACTCTTATGAT CAAAAAAGGCCA C[A/T]TTTTTTAA GATTGTATTACTT GATT	A	T			SILENT-NONCODING	polymerase	Human Gene Similar to SWISSNEW-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.|pcls:SWISSPROT-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5
2621	cg43969348	422	TAGCTGCTAACA ATGGCTTGGGTC T[C/G]AGGGCAA CCCAGGTCCCCA TGGTGC	C	G			SILENT-NONCODING	polymerase	Human Gene Similar to SPTREMBL-ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SIII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa.	3.90E-59	16
2622	cg43924683	161	TACAAAACCCCC CATCCAGATATA T[T/gap]CACGTTA ACAATTCTGAGA TAACTG	T	gap			SILENT-NONCODING	polymerase	Human Gene Similar to TREMBLNEW-ID:G300899 A1 REPLICATIVE POLYMERASE ACCESSORY PROTEIN 36 KDA SUBUNIT - HOMO SAPIENS, 325 aa.	1.40E-54	3 (3q27)
2623	cg42534568	104	CGAGGGGATGC GCGCCAGCAAC CCC[C/gap]AGCT CTCCCCAGAGAG GGGCCGGCC	C	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2624	cg42534568	132	CTCTCCCCAGAG AGGGGCCGGCC GA[G/C]GCTGGA GCGGAGCCTGA CGCCAGGC	G	C			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2625	cg42534568	2529	GGTAAGTGGCTT TTTGTACTGTAG T[T/gap]CAGATA GAGATATTTTGG GTATATT	T	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)

2626	cg42534568	2546	ACTGTAGTTCAG ATAGAGATATTTT [G/gap]GGTATAT TTTCAAGATACA TGTTGT	G	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2627	cg42534568	2556	AGATAGAGATAT TTTGGGTATATTT [T/gap]CAAGATA CATGTTGTATTTA TGGAA	T	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2628	cg42534568	2585	GATACATGTTGT ATTTATGGAAGA A[A/T]GTGTTGGT CCTGATGGTTTT TCTGT	A	T			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2629	cg42534568	2617	GTCCTGATGGTT TTTCTGTGTTACT [T/gap]ATATTAGA GTCAGAGATCTT GGTAT	T	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2630	cg42534568	88	TGACGTCAGGG CCAAGCGAGGG GAT[G/gap]CGCG CCAGCAACCCCC AGCTCTCCC	G	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2631	cg44938709	758	AGACCGCGAAC CGGGAGGAGCG CGG[G/gap]CCCC ACCCTAAAGAGG GCGCAGCCG	G	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P17658 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (HBK2) - HOMO SAPIENS (HUMAN), 529 aa.	1.00E-287	12 (12p13)
2632	cg42937321	132	GGTGCCCACAC GCTGGTGAACCA CG[G/gap]CTACG CGGAGCCCCGC CGCAGGCCG	G	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

2633	cg42937321	137	CCACACGCTGGT GAACCACGGCTA C[G/gap]CGGAGC CCCGCCGCAGG CCGCGAGC	G	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2634	cg42937321	149	GAACCACGGCTA CGCGGAGCCCC GC[C/gap]GCAGG CCGCGAGCTGC CGCCCGACA	C	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2635	cg42937321	151	ACCACGGCTACG CGGAGCCCCGC CG[C/gap]AGGCC GCGAGCTGCCG CCCGACATG	C	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2636	cg42937321	1820	CTTGGTCTGCCT ATGCCCTTGTTT T[gap/T]ATACATT TCCAGACCATTC ATCAAG	gap	T			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2637	cg42937321	3084	ACCTTACTACAA GGGACCTTCAG GC[C/gap]TTTTCT CTTTAAAAAAAA AATACA	C	gap			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

2638	cg43333426	1740	TCAGGACAGAGC CAACCCTGGCTC C[A/G]TGGACCTT CTGGAGGAAGG TGGGGG	A	G			SILENT-NONCODING	potassium_channel	Human Gene SWISSNEW-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.|pcls:SWISSPROT-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.	4.40E-241	
2639	cg40991967	78	CAACAGGGCCTC GGGTACCCTCAC C[C/T]AGCATATC CAAACTCTTGCA TCAAA	C	T			SILENT-NONCODING	potassium_channel	Human Gene SWISSPROT-ID:P48048 ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 1 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 1) (ATP-REGULATED POTASSIUM CHANNEL ROM-K) (KIR1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.80E-205	11 (11q24)
2640	cg43008113	161	CTGCGGCGTTG GCCTTGGCTTTG GC[C/T]TTGGCG GCGGCGGTGGA GAAGATGC	C	T			SILENT-NONCODING	potassium_channel	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.|pcls:TREMBLNEW-ID:G2811120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.80E-180	1
2641	cg43008113	1806	AGTGTAGTTCTG AAACTAAGACTA T[A/gap]GATATTT TGTTTCTTTTGAT TTCTC	A	gap			SILENT-NONCODING	potassium_channel	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.|pcls:TREMBLNEW-ID:G2811120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.80E-180	1

2642	cg43917554	1297	GTCCCCACTCAA CTGACTCATACC T[G/T]TTTCCGGC TGCATCACTATG TGCCC	G	T			SILENT-NONCODING	potassium_channel	Human Gene Similar to SPTREMBL-ID:Q16558 MAXIK POTASSIUM CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 191 aa.	1.80E-100	5
2643	cg43262191	2044	TCTGACCCCACC CTGGGCCACTG CC[C/gap]TGCTC CAGAGAGTGGA CCTTGACTC	C	gap			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.|pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2644	cg43262191	3156	TTCCCATTTTCTC AGCCTCTTCTCA[C/gap]TGCCTCCA GAGAGGTGGGT GCCTGG	C	gap			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.|pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2645	cg43262191	3174	CTTCTCACTGCC TCCAGAGAGGTG G[G/A]TGCCTGG GTTGAGAGACAC AGCTGC	G	A			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.|pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2646	cg43262191	3258	AAGGAGGTCATT CATCAACAAATA T[A/G]TTTATTGG AGACCGACTTTG TGCAA	A	G			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.|pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3

2647	cg43262191	3914	ATGGCAATTTAA CCACATTTGGAA G[G/gap]CACTGC CTTCAGCTGAGT TTATGAA	G	gap			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.|pcls:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2648	cg43951366	174	CCCTCAGACAGC AAAGCCTACCCC C[gap/C]GCGCCG CGCCCTGCCCG CCGCTGCG	gap	C			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)

2649	cg43951366	197	CCCGCGCCGCG CCCTGCCCGCC GCT[G/C]CGATG CTCGCCCGCGC CCTGCTGCT	G	C			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)
2650	cg43951366	198	CCGCGCCGCGC CCTGCCCGCCG CTG[C/G]GATGC TCGCCCGCGCC CTGCTGCTG	C	G			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)

2651	cg43951366	2441	TTTGAAATTTTAA AGTACTTTTGGT[T/C]ATTTTTCTGT CATCAAACAAAA ACA	T	C		SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)
2652	cg43951366	2676	CTTGGATTTAAA TCTGTAAAATCA G[A/T]AGAAATTT TACTACAATTGC TTGTT	A	T		SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)

2653	cg43951366	2677	TTGGATTTAAAT CTGTAAAATCAG A[A/T]GAAATTTT ACTACAATTGCT TGTTA	A	T			SILENT-NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)
2654	cg43306254	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCAGC CGCGGTAAAC	G	gap			SILENT-NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2655	cg43306254	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCCCTCCCG CTGCGGCTC	G	gap			SILENT-NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2656	cg43306254	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C/gap]TGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT-NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)

2657	cg43306254	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT-NONCODING	prostaglandin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2658	cg42913398	319	TACAACATAAAA AATAAAATAAGC A[A/G]ACTGTCTG AGGGGTTTATAT AAGGT	A	G			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:O00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa.	0.00E+00	2
2659	cg43916732	1438	GCTGCGTCCCA GGACTGAGACG CAG[G/gap]CCAG CCCCGGCCCCT AGCCCTCAGG	G	gap			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2660	cg43916732	1448	AGGACTGAGAC GCAGGCCAGCC CCG[G/gap]CCCC TAGCCCTCAGGC CTTCTTTCT	G	gap			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2661	cg43916732	1500	ATCCAAATAAAT GTTTCTTAATGA G[A/G]AAAAAAAA AAAAAAAAAAAA AAAAA	A	G			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2662	cg43967594	641	TTGCTAGGTATA ATTTTATTTTATA[T/gap]AAAAAGTG TTTCTGTGATTCT TCAG	T	gap			SILENT-NONCODING	protease	Human Gene TREMBLNEW-ID:G2738915 SERINE PROTEASE - HOMO SAPIENS (HUMAN), 529 aa.	6.10E-239	2
2663	cg43922779	2882	TTTTTAAAACTAA CCAAAAAAGGCC [G/gap]GGTGCTG GGATTACAGGCA TGAGCC	G	gap			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:O00232 PROTEASOME SUBUNIT P55 - HOMO SAPIENS (HUMAN), 456 aa.	4.40E-236	17

2664	cg43986296	540	CATCTGCTCTGC AGTCCTGCCGCA G[G/gap]ATTCCC TAGTGAAGCAGC TCAGGCC	G	gap			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
2665	cg43986296	833	CTTCTCAACTTAT ATGTGGGAAGG G[G/gap]TCCCCC ATGCTTGGGGGA CCTAGGC	G	gap			SILENT-NONCODING	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
2666	cg44932353	143	TTCAGCCACACT GACGGCTCTGA GC[C/gap]AGAGC CACCTCCTGGCC CCACTGGT	C	gap			SILENT-NONCODING	protease	Human Gene TREMBLNEW-ID:G2880036 SIMILAR TO FURIN-LIKE PROTEASES - HOMO SAPIENS (HUMAN), 286 aa.	1.10E-155	3
2667	cg43306871	108	GTGTTAAGCCTT ACATGACAATCA C[C/gap]ATGAAG ATTTACATACAC ATGTTAT	C	gap			SILENT-NONCODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.|pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2668	cg43306871	230	AGGTTCAGAGAG GGCACTTGGCTT G[C/gap]CCAAAG TCACACAGCAGG GAGTGGC	C	gap			SILENT-NONCODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.|pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19

2669	cg43306871	232	GTTCAGAGAGG GCACTTGGCTTG CC[C/gap]AAAGT CACACAGCAGG GAGTGGCAG	C	gap			SILENT-NONCODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.|pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2670	cg43306871	246	CTTGGCTTGCCC AAAGTCACACAG C[A/G]GGGAGTG GCAGAGGAAGT CAGGTTG	A	G			SILENT-NONCODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.|pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2671	cg43306871	313	GCTCTCAGAGGC TGGGTGATGACC G[G/A]CTTCCTG GCTTCTCTGGAA TAAACC	G	A			SILENT-NONCODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.|pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19

2672	cg43923853	133	ACACTTTAAGATACCATTACATGCT[A/G]TGTGTATTTACAAAAGTTACAGGTC	A	G			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.|pcls:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4
2673	cg43923853	190	GAAAAAAGAAACTGTCATTGACAAA[T/C]GCGAGCTCATTTTTTGAGCAACAAG	T	C			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.|pcls:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

2674	cg43923853	295	CTCCGCACCTGC TGAGGCCTGGA GC[C/gap]TGCCT CCCGGGCTGAG GGCTCAGCT	C	gap		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.|pcls:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4
2675	cg43923853	312	CCTGGAGCCTG CCTCCCGGGCT GAG[G/T]GCTCA GCTCTGGCCTCC GGCTGGAT	G	T		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

2678	cg42918089	1172	TTTATGGTGTGA CTGTGTCTTATT C[gap/C]ATCTATA CTTGCAGTGGGT AGATGT	gap	C		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2679	cg42918089	1178	GTGTGACTGTGT CTTATTCATCTAT [gap/G]ACTTGCA GTGGGTAGATGT CAATAA	gap	G		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2680	cg42918089	1179	TGTGACTGTGTC TTATTCATCTATA [gap/G]CTTGCAG TGGGTAGATGTC AATAAA	gap	G		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2681	cg42918089	1182	GACTGTGTCTTA TTCATCTATACTT [gap/T]GCAGTGG GTAGATGTCAAT AAATGT	gap	T		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2682	cg42918089	1183	ACTGTGTCTTAT TCATCTATACTT G[gap/T]CAGTGG GTAGATGTCAAT AAATGTT	gap	T		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2683	cg42918089	1188	GTCTTATTCATCT ATACTTGCAGTG[gap/C]GGTAGAT GTCAATAAATGT TACATA	gap	C		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2684	cg42918089	1189	TCTTATTCATCTATACTTGCAGTGG[gap/C]GTAGATGTCAATAAATGTTACATAC	gap	C			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2685	cg42918089	1230	TGTTACATACACAAATAAATAAAAT[G/A]TTTATTCCATGGTAAATTTAAAAAA	G	A			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2686	cg42918089	1235	CATACACAAATA AATAAAATGTTTA [T/G]TCCATGGTA AATTTAAAAAAAA CCG	T	G		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2687	cg42918089	1236	ATACACAAATAA ATAAAATGTTTAT [T/G]CCATGGTAA ATTTAAAAAAAAC CGC	T	G		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2688	cg42918089	1251	AAATGTTTATTCCA[A/C]AAAAAACCGCCGATACTGACGGGC	A	C			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
2689	cg42918089	1252	AATGTTTATTCCA[A/C]AAAAACCGCCGATACTGACGGGC	A	C			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
2690	cg43074055	1055	CTCTTCCCCGAA[G/gap]GACGGCCCCACCCGTCCCCCACA	G	gap			SILENT-NONCODING	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.70E-138	19 (19p13.3)

2691	cg43990989	110	ATTCCATGTATG TCATAGGTGTGA A[A/gap]CCTTAAA TCTTTCCAACAG CCACTG	A	gap			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:Q92876 PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN) (ZYME) (SP59) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SPTREMBL-ID:Q92876 PROTEASE M PRECURSOR - HOMO SAPIENS (HUMAN), 244 aa.	7.50E-136	19
2692	cg43990989	235	GGGGACACCGA CAGTAAGCAGCG GA[G/gap]CTGGG ATTCCAGACACG TGGCTGGG	G	gap			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:Q92876 PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN) (ZYME) (SP59) - HOMO SAPIENS (HUMAN), 244 aa.|pcls:SPTREMBL-ID:Q92876 PROTEASE M PRECURSOR - HOMO SAPIENS (HUMAN), 244 aa.	7.50E-136	19
2693	cg43967243	1072	GCTGGAACCAC GGGACATGTTGG TA[G/C]AAGCACT ACTTTAAACACA ATCCCT	G	C			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.|pcls:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130	

2694	cg43967243	209	ATATAGAGTCCT AACCACTTCGGT G[G/gap]TAGGAG GAGTGGGAGAG GCTCCTTT	G	gap		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.[pcls:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130		
2695	cg43974374	496	GGTCACTGTGTC CGTATTACCAAT G[A/G]CAGTCAC CCCAAGAAACAC AAGCAG	A	G		SILENT-NONCODING	protease	Human Gene Homologous to SPTREMBL-ID:Q16242 PROTEASOME SUBUNIT MB1 - HOMO SAPIENS (HUMAN), 215 aa (fragment).	7.40E-113	14 (14q11.2)	
2696	cg2510140	22	CAAGCAGATAGG ACACTGGAA[A/G] AAGGAATGCCCA TTAAAACCAGAA G	A	G		SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P03356 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - AKV MURINE LEUKEMIA VIRUS, 1196 aa.[pcls:SWISSPROT-ID:P03356 POL POLYPROTEIN (PROTEASE (EC 3.4.23.); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) - AKV MURINE LEUKEMIA VIRUS, 1196 aa.	1.90E-105		

2697	cg43917011	186	AACTCTCAATGCTTAACCATTTTCA[G/A]TTGCCAGGAAAGAGGTAGAAATATC	G	A			SILENT-NONCODING	protease	Human Gene Homologous to SWISSNEW-ID:P49662 CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICE(REL)-II) - HOMO SAPIENS (HUMAN), 377 aa.|pcls:SWISSPROT-ID:P49662 CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICEREL-II) - HOMO SAPIENS (HUMAN), 377 aa.	1.50E-103	11
2698	cg43930253	1288	ATATTGGATGGCGAGGACAGCGTGG[T/C]ACTGGCTGCGAGTGTTCCTGAGAGT	T	C			SILENT-NONCODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B-LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2699	cg43930253	1349	ATGACTTATGACACTTGCACAGCAT[G/gap]GCTCTGCCTCACAATGATGCAGTCA	G	gap			SILENT-NONCODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B-LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2700	cg43930253	1350	TGACTTATGACACTTGCACAGCATG[G/gap]CTCTGCCTCACAATGATGCAGTCAG	G	gap			SILENT-NONCODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B-LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2701	cg43930253	1400	GCCACCTGGTGAAGAAGTGACCTGC[G/A]ACACAGGAAACGATGGGACCTCAGT	G	A			SILENT-NONCODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B-LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20

2702	cg43947922	934	TAGATTTGAGAC AACTAGCCTGTT A[C/T]TCAGCCCA ATATCCCCCCAT GGTTT	C	T			SILENT-NONCODING	protease	Human Gene Similar to SWISSNEW-ID:P28070 PROTEASOME BETA CHAIN PRECURSOR (EC 3.4.99.46) (MACROPAIN BETA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX BETA CHAIN) (PROTEASOME CHAIN 3) (HSN3) (HSBPROS26) - HOMO SAPIENS (HUMAN), 264 aa.	1.10E-97	
2703	cg43104740	2154	ACATGGATGAGC ACACACACCA A[gap/G]TGCGCA CACACACCGATG TACACAC	gap	G			SILENT-NONCODING	protease	Human Gene Similar to SWISSPROT-ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	5.00E-94	13
2704	cg43297588	23	GGCACAGCATG CGGGGCGTGTG[C/G]GCCCCCCCC GGTGTCCGCCCT GCTGT	C	G			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2705	cg43297588	24	GGCACAGCATG CGGGGCGTGTG C[G/C]CCCCCCC GGTGTCCGCCCT GCTGTC	G	C			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2706	cg43297588	26	GGCACAGCATG CGGGGCGTGTG CGC[C/G]CCCCC GGTGTCCGCCCT GCTGTCGG	C	G			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2707	cg43297610	153	CAGCTGAGCAG GGTGGCTGTTCC TC[G/T]GCTGGAT TAGGGCTGAATC TGTGGG	G	T			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)

2708	cg43297610	2707	GCCGGACATCCCAGGCACACGTGTG[C/gap]GCCACCTTCAGCAGGCATTCGGGTG	C	gap			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)
2709	cg43297610	2760	GGGCTGGTGGCTCATCAGGCCTGGG[C/gap]CCCACACTGACAAGCGCCAGATACG	C	gap			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)
2710	cg43917924	315	ATTTTGTCTCACTCGATTCAGACAC[T/G]TAAATGGGAGTTTTCAGTTTATCCT	T	G			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	1.80E-81	3 (3q21)
2711	cg43921680	347	GCCAAGTCATTTAAAAAGGATTTAG[G/gap]CCACTGCCTTTTTCTGAGGGAGGAG	G	gap			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2712	cg43921680	612	CATGTTGTTAAACAGTAGAGGAGCC[A/G]GGGACTCTGTCTCCATTCTCTCATC	A	G			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2713	cg43921680	689	AAAAAAAAACAAAAAAACACAACAA[C/gap]AAAAAAACTGTCCTCTGAGGAGGCA	C	gap			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2714	cg42033569	513	GCTGTCCATTAGTAGAAGAGCAAGA[G/A]AGCCTTGGATGTCAACGCCTCGCTC	G	A			SILENT-NONCODING	protease	Human Gene Similar to SPTREMBL-ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-72	

2715	cg44031287	300	TTCACAGGTGCCAGAGCTTAGAGGT[G/T]TCACAGGCACCGGGGTGGCTCCTGC	G	T			SILENT-NONCODING	protease	Human Gene Similar to TREMBLNEW-ID:G2736064 UBIQUITIN SPECIFIC PROTEASE 41 - GALLUS GALLUS (CHICKEN), 357 aa.	8.10E-67	1
2716	cg43276961	1111	GATGACAAATACTGGTTAATTAGCA[A/G]TTTAAGACCAGAGCCAAATTATCCC	A	G			SILENT-NONCODING	protease	Human Gene Similar to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2717	cg43276961	1343	GGCCTAAAATTGATGCAGTCTTCTA[C/T]TCTAAAAACAAATACTACTATTTCT	C	T			SILENT-NONCODING	protease	Human Gene Similar to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)

2718	cg43276961	1686	AGTTTGAAAATA GTTACCTTCAAA G[G/gap]CCAAGA GAATTCTATTTG AAGCATG	G	gap			SILENT-NONCODING	protease	Human Gene Similar to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2719	cg43276961	1693	AAATAGTTACCT TCAAAGGCCAAG A[G/T]AATTCTAT TTGAAGCATGCT CTGTA	G	T			SILENT-NONCODING	protease	Human Gene Similar to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2720	cg43069905	417	TCAGCGCCCTCC ACAGTGGCAGTG C[C/gap]AGCTTG GAATCCCGCTTC CGGTTGT	C	gap			SILENT-NONCODING	protease	Human Gene Similar to SWISSPROT-ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	1.30E-57	13
2721	cg43316919	1645	AAGGAAAGGAGT ATTGGAAATTCA A[A/gap]CAACCA GATACTCAAGGT AGAACCT	A	gap			SILENT-NONCODING	protease	Human Gene Similar to SWISSPROT-ID:P22757 HATCHING ENZYME PRECURSOR (EC 3.4.24.12) (HE) (HEZ) (ENVELYSIN) (SEA-URCHIN-HATCHING PROTEINASE) - PARACENTROTUS LIVIDUS (COMMON SEA URCHIN), 587 aa.	8.10E-56	

2722	cg44028327	3348	TGGATGCATTTG AACCTCTGAGTT T[G/C]TCTTTCAT TTTAAATATTGTC TGTT	G	C			SILENT-NONCODING	proteaseinhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
2723	cg44028327	3540	CAAGGGTCGAC CCCCAAAGGCA GGG[gap/G]CAGA GCCAGCATCTGA GAGGGAGGT	gap	G			SILENT-NONCODING	proteaseinhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
2724	cg43979831	1589	GTTGGGGACAA GGATGACACCGA AG[G/gap]TCCAG GAGTCCAGGACA GCAGGTGC	G	gap			SILENT-NONCODING	proteaseinhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
2725	cg43979831	1628	GACAGCAGGTG CTGGCCGGTGG GGA[G/A]CGGGG AGGGGCACTGA GATGGGCAG	G	A			SILENT-NONCODING	proteaseinhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
2726	cg43920929	320	GGAAAAGAATTT AAAAGGCAAATA A[gap/T]TTTTTTT TTCATAAAAAGT AAAAGC	gap	T			SILENT-NONCODING	proteaseinhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
2727	cg43268468	1394	TGCTGTCGGGGT CTGGGGAGCCC TC[C/gap]TCCGG GGGGCTGGCAG GGTTCTGGC	C	gap			SILENT-NONCODING	proteaseinhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188	17 (17p13.3)
2728	cg43268468	1560	CTGAGGGGGCT CCAGCCAGCACA GA[G/T]CTTTTTT TGCTGCCTTCTA ATCCAG	G	T			SILENT-NONCODING	proteaseinhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188	17 (17p13.3)

2729	cg43932980	93	GAGTTATAGCTA CCCCGGCCGCG GA[G/gap]CCGGC TCACTGCACTAC CCCCGCCC	G	gap			SILENT-NONCODING	proteasei nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20
2730	cg43932980	3021	GAGAAACACAGT CATTGTCTTAGG T[G/A]TTCTATGG GAGGAAGTGAAT AGAGC	G	A			SILENT-NONCODING	proteasei nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20
2731	cg43932980	67	GCAAGAACCAGC GCAAGAGGGAA GC[G/A]GAGTTAT AGCTACCCCGG CCGCGGA	G	A			SILENT-NONCODING	proteasei nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20

2732	cg43990892	159	AAAATAATTCATACAAAAATTTCAA[G/A]CATCACTGCTGTAGATATTCCTCCA	G	A		SILENT-NONCODING	reductase	Human Gene SWISSNEW-ID:P54886 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] - HOMO SAPIENS (HUMAN), 795 aa.|pdb:SWISSPROT-ID:P54886 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) (CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) / GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)) - HOMO SAPIENS (HUMAN), 795 aa.	0.00E+00	10 (10q24.3)

2733	cg43990892	446	AAATCTTTCCTTT[A/G]CATGTGAAA GAAATAAAATGT GAAA	A	G			SILENT-NONCODING	reductase	Human Gene SWISSNEW-ID:P54886 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] - HOMO SAPIENS (HUMAN), 795 aa.|pcls:SWISSPROT-ID:P54886 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) (CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) / GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)) - HOMO SAPIENS (HUMAN), 795 aa.	0.00E+00	10 (10q24.3)
2734	cg44002608	282	ATTCAAATTATTA TTATTTTTTTTT[gap/T]ACAAAGAAA TAAACCTGTAAA GGAT	gap	T			SILENT-NONCODING	reductase	Human Gene SPTREMBL-ID:Q94511 75KDA SUBUNIT NADH:BIQUINONE REDUCTASE PRECURSOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 653 aa (fragment).	4.60E-223	2
2735	cg43969711	722	CAAATAAATCAA GCTATTATCGCC T[T/C]GTGAGTAC AAACAATGTTTAT TTGT	T	C			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)

2736	cg43969711	733	GCTATTATCGCCTTGTGAGTACAAA[gap/A]CAATGTTTATTTGTTTGTAAAGTGC	gap	A			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)
2737	cg43941472	1139	GGGGACAAAGCAGCGTCTGGCTCGA[G/gap]TGGAAGCGTCCAAACCTGCTTTTCC	G	gap			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2738	cg43941472	1208	TTCCGTCAGAGCTTCTGGCTGCTCC[T/A]GAATGGTGGAATGCTGTGTCCTCTC	T	A			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2739	cg43941472	1222	TGGCTGCTCCTGAATGGTGGAATGC[gap/C]TGTGTCCTCTCTTCTGTCTCCTGCT	gap	C			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2740	cg43941472	1247	CTGTGTCCTCTCTTCTGTCTCCTGC[T/C]GCCTGGAGGCTTCGGGGCTCTCCCG	T	C			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2741	cg43941472	1281	GCTTCGGGGCTCTCCCGCCTGCCTT[G/C]TCGGGGCCCAGACGCAAGGCACCGA	G	C			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2742	cg43941472	1440	TCTTTTTTAAAAGAAGATGGTTTCA[gap/G]CTTTAATATAATGCTATTATCTTAA	gap	G			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)

2743	cg43941472	1474	TAATGCTATTATC TTAAGACTTAAA[A/G]AAGTTGCTG GAGTTTGTATTT CCAG	A	G			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2744	cg43941472	1475	AATGCTATTATCT TAAGACTTAAAA[A/G]AGTTGCTGG AGTTTGTATTTC CAGG	A	G			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2745	cg43987538	115	ACTTTATTACACA TTATTATGTTAC[G/A]AGACAAATG CAGATAATTCTT AATT	G	A			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
2746	cg43987538	86	TTTTTTTTTTTTT TTTTAATTTTCT[A /G]TAGACTTTATT ACACATTATTAT GT	A	G			SILENT-NONCODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
2747	cg40312187	2424	AGGATGATGTAG ATTACTGAAAAA T[A/G]CAAATTGC AATCATATAAATA AGTG	A	G			SILENT-NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P31213 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2) - HOMO SAPIENS (HUMAN), 254 aa.	5.70E-138	2 (2p23)
2748	cg43918176	50	TTTTTTTTTTTTT CTTTTTTTTTTTT[T/ C]TGTGAGAAAAA GAGACTTTATTA GG	T	C			SILENT-NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3-HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM-ASSOCIATED AMYLOID BETA-PEPTIDE BINDING PROTEIN) (SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2.00E-133	X

2749	cg43927549	1010	TGGGCATCACGTAAGCAGCACACTA[G/C]GAGGCCCAGGCGCAGGCAAAGAGAA	G	C			SILENT-NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
2750	cg43995873	386	GGGGCGGGGCCTCGCCTGCACAAAT[A/G]GGGACGAGGGGGGCGGGGCGGCCAC	A	G			SILENT-NONCODING	reductase	Human Gene Similar to SWISSNEW-ID:P00374 DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) - HOMO SAPIENS (HUMAN), 186 aa.|pcls:SWISSPROT-ID:P00374 DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) - HOMO SAPIENS (HUMAN), 186 aa.	1.90E-98	5 (5q11.2)
2751	cg43936109	399	TCCAATAAGCAAATGGACATTGGTC[C/gap]ATTTGGCATGTGTAATTCTCTTTTT	C	gap			SILENT-NONCODING	ribosomal prot	Human Gene SWISSPROT-ID:P49406 PUTATIVE 60S RIBOSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	2.50E-151	2
2752	cg43982087	1708	TTAGTGGCTTCAAAGGCCCAGCTGA[C/A]ACCCTCCACAGCCTAAGGGGTGTCC	C	A			SILENT-NONCODING	ribosomal prot	Human Gene Similar to SWISSPROT-ID:P17103 HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION - HALOBACTERIUM CUTIRUBRUM, 370 aa.	2.70E-67	17
2753	cg43982087	1759	TAAAGTGCCTCCCCCTGTATTCCCC[C/T]TCCCAGGGCAGCCCCTGCCCAGCAC	C	T			SILENT-NONCODING	ribosomal prot	Human Gene Similar to SWISSPROT-ID:P17103 HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION - HALOBACTERIUM CUTIRUBRUM, 370 aa.	2.70E-67	17

2754	cg44923577	838	TCCCAAGAAGAA GGTCAAATAAGG T[T/G]GTTCTTTC CTTGAAGGGCAG CCTCC	T	G			SILENT-NONCODING	ribosomal prot	Human Gene Similar to SPTREMBL-ID:Q95260 UBIQUITIN/RIBOSOMAL FUSION PROTEIN - SUS SCROFA (PIG), 128 aa.	1.10E-65	19 (19p13.1)
2755	cg42845774	566	TAAATGAAGAC ATTTGGGTGTTT C[A/G]TGTCAGTG AATTATCTTTTCT CTTG	A	G			SILENT-NONCODING	ribosomal prot	Human Gene Similar to TREMBLNEW-ID:E1284377 DJ262D12.2 ((MITOCHONDRIAL/CHLOROPLAST 30S RIBOSOMAL PROTEIN S14)-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 128 aa.	1.70E-65	1
2756	cg43255045	5967	ATATCTTGACAC CTGCCAAAGCTT C[G/C]AGCACGG GAAAATGAGAAA CACTGG	G	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0.00E+00	1
2757	cg43255051	624	AGGAAGTTTTTA TGCAGAGGTCAC T[C/A]CCCCTGCA CTATTCAAGGGT TATAA	C	A			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0.00E+00	1
2758	cg43966202	19	TTTTTCGTCGTTT TTTTT[G/T]TAATA AAGACACTGCTT TTATTTAG	G	T			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q14118 DYSTROGLYCAN PRECURSOR (DYSTROPHIN-ASSOCIATED GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 895 aa.	0.00E+00	3
2759	cg43973080	1686	GGCAAAGGCTC CCAGCTGTAAGG CT[G/A]GTGTGCA ACATCTACTTTAA CAGAC	G	A			SILENT-NONCODING	struct	Human Gene TREMBLNEW-ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa.	0.00E+00	6
2760	cg43957646	1766	AGAAAAGTGAAA CAAAACCATAAA C[A/G]AAGCAGC GGGGTTCACGA CGCTAAA	A	G			SILENT-NONCODING	struct	Human Gene SPTREMBL-ID:O00185 BETA CATENIN - HOMO SAPIENS (HUMAN), 596 aa.	0.00E+00	10

2761	cg43957640	2076	AAAGGAATGAAG AGGGTGTGAGG CC[C/gap]AATGG GGCTGGGTGGG AGGCGGTGC	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P13796 L-PLASTIN (LYMPHOCYTE CYTOSOLIC PROTEIN 1) (LCP-1) (LC64P) - HOMO SAPIENS (HUMAN), 627 aa.	0.00E+00	13 (13q14.1)
2762	cg44033566	6709	TGACGTTATTAG TTTTGTTTTACCT [gap/G]AATGTAA TAAATTTTATTGT ATAAA	gap	G			SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.|pdb:SWISSPROT-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0.00E+00	14 (14q22)
2763	cg43957486	3192	AAACAAAGGTTG AGATGTAAAAGG T[A/G]TTAAATTG ATGTTGCTGGAC TGTCA	A	G			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
2764	cg43957486	3400	ATGTTCAGAAGG TTGCTCTAGATT G[A/C]GAGAAGA GACAAACACCTC CCAGGA	A	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
2765	cg43249606	20	TTTTTTTTTTTTT TTTTTG[T/A]GAG AAGCTGAGCTGT TTAATCACCT	T	A			SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.|pdb:SWISSPROT-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.	0.00E+00	
2766	cg44918439	2202	TTTTTTTCTTTT TCTTTTTTTTTT[g ap/T]CTGTTGAAG ATTAACACTAATT ATC	gap	T			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)

2767	cg44918439	2375	TCACATTTTCTCAGTGTGCCCTTCT[C/G]TTATCTGCCATGTCCATAGCCATAA	C	G			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
2768	cg43967978	1187	AGTTCAGAATTCTAGGCCCAAAAGG[G/gap]TGCAACACCCTTCAACCAGTTTCAG	G	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2769	cg43967978	1522	TAGAGAAGTAAAAGCAACTCAGGCG[gap/G]ATATGAATTCAAACCTCAGTGTAGA	gap	G			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2770	cg43967978	1582	AAGTCGGTACAGTGTCCAGGCACGC[C/gap]GTCCCGGAGACGGAGGAAGTGACTA	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2771	cg43967978	1688	GGGAGGGCGGGTCTAAAAGGCAGGG[G/gap]CAGTCGCCAGGCCTAGGGCACTGGA	G	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2772	cg43967978	1716	GTCGCCAGGCCTAGGGCACTGGAAG[G/A]GTAGGAGGAGCACAGAGAACCTTCC	G	A			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2773	cg43967978	693	AGACCCCAGCACACTCGGCTTCTGC[C/gap]AGGAGGCCAGTGGAGTGGTTTGGAC	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	

2774	cg43967978	814	CTTGGTAAAGAG CTCTGGGGGGTT T[C/gap]CCCAGA GGAGCCTGTCC CTCTGCCC	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2775	cg44034221	1989	TGCTGTACCTCG ATCTGAATCTGC C[G/gap]GGGCCC CAGCCCACTCCA CCCTGCC	G	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2776	cg44034221	1991	CTGTACCTCGAT CTGAATCTGCCG G[G/gap]GCCCCA GCCCACTCCACC CTGCCAG	G	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2777	cg44034221	1992	TGTACCTCGATC TGAATCTGCCGG G[G/gap]CCCCAG CCCACTCCACCC TGCCAGC	G	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2778	cg44034221	2020	CCAGCCCACTCC ACCCTGCCAGCA G[C/gap]TTCCAG CCAGTCCCCACA GCCTCAT	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2779	cg44034221	2096	CTATCTTCCCCC ACCCCCAGCTAC C[C/gap]ATAGGG GCTGCAGAGTTA TAAGCCC	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	

2780	cg43980812	238	TAAACTCGAGGGATTATTATTTCTT[G/A]ATTGGAGAAAGAGAAGACAGCATTT	G	A			SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:Q15654 THYROID RECEPTOR INTERACTING PROTEIN 6 (TRIP6) (OPA-INTERACTING PROTEIN 1) (ZYXIN RELATED PROTEIN 1) (ZRP-1) - HOMO SAPIENS (HUMAN), 476 aa.	2.90E-272	7
2781	cg43931165	218	CGGCTCCCGAGTCTTGGAGAAGAGC[A/G]CGAGAACCTAGACCGCCCCCGAAGT	A	G			SILENT-NONCODING	struct	Human Gene SPTREMBL-ID:Q14704 MRNA (KIAA0092) FOR ORF (SMOOTH MUSCLE MYOSIN-RELATED) - HOMO SAPIENS (HUMAN), 474 aa.	3.00E-242	11
2782	cg43987609	996	GCACTCCATAATAACTGGAATCCCA[C/T]GAGTGTGTATGCCAAGTCTCATGAG	C	T			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.10E-226	2
2783	cg42491601	1485	TGGAAGAAAATATCTAAATAGCTAC[C/gap]AGAAGGAGATGCTGCTGAGGTTTTG	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.40E-215	17
2784	cg42491601	1694	AAATTGCCTGCAAAAATGAAATCCA[G/A]TGAGCACTAGAATATTTAAAACATC	G	A			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.40E-215	17
2785	cg43947066	119	TTTAGCTTTCCACTGATATCTCAAG[A/C]TACTTTCCAGATATTAACAGTACTC	A	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2786	cg43947066	1685	CTTAAGCTCTTTTAAATCTGTAATT[T/C]GAATTACCCAAAGGATTTTTAAATG	T	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2

2787	cg43947066	2228	ATACCACCTAGTGTGCTAAAGACTA[C/T]GACTAGCAGCATTAGAGCAGTAAAG	C	T			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2788	cg43947066	378	TTTTTAAAACAGAATTTTTTTTTTT[T/gap]CCTGAGGGACTCATACTTGACAACT	T	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2789	cg43947066	74	TTATTTTCTCAATCAAAATGAAGTA[T/C]TTCATGTTAATTTAGACTGTTTAGC	T	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2790	cg43947066	843	CCCAAGATCTAGTACGGGCTATTCA[T/G]GGTTCTGAGGCATGTCCAGCATGCA	T	G			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2791	cg43963568	140	CAGATGCTTTCTGAAGAGCCCTGGG[G/gap]CAGGGGGCAGCCTTGCCCCTCACAT	G	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2792	cg43963568	230	GGATTCCAGGTCTGGAGCCAAGAAC[G/C]TAGTCCAAAGATCCCCTCTTCCCTT	G	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2793	cg43963568	2870	CAGGAGGGAGGTCCACTGCATTTTG[T/gap]CTCTCAAGTTGAACTTTTCAGAGAA	T	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)

2794	cg43963568	2872	GGAGGGAGGTC CACTGCATTTTG TC[T/gap]CTCAA GTTGAACTTTTC AGAGAAGT	T	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2795	cg43963568	317	GGATGTGATGGC ATCTGGGCAGAG C[C/gap]TATACTT GGGCTAACTCTC CTCCAA	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2796	cg43983086	139	AGCCTAGGATGG TCAGCAGCAAGG T[C/G]TCCCGGG GGATGGCTTACC TCCCTC	C	G			SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.|pcls:SWISSPROT-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.|pcls:TREMBLNEW-ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10

2797	cg43983086	304	TAGTGGTCAACC CCAGGCCTCAG GC[gap/A]CATCA CCACTGCAGGTA GTTCATCG	gap	A		SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.|pcls:SWISSPROT-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.|pcls:TREMBLNEW-ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10
2798	cg43983086	432	ACACAGGCAGTT CCTCGCAAACAC T[C/A]CGACTCAA GAAAGCGAGTTT TAAAG	C	A		SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.|pcls:SWISSPROT-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.|pcls:TREMBLNEW-ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10

2799	cg43983086	433	CACAGGCAGTTC CTCGCAAACACT C[C/A]GACTCAAG AAAGCGAGTTTT AAAGT	C	A			SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.|pcls:SWISSPROT-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.|pcls:TREMBLNEW-ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10
2800	cg43923264	1291	CTGTTCAGTGCC GACCTGCGCCAA T[C/G]CCGCCAT GCTCAGGAGCC ACCAGCA	C	G			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2801	cg43923264	1364	GGCCGGAAGGC TAGATGGGGCAC CC[T/A]GGACAAA GAAATTCCCCAA GCACCT	T	A			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2802	cg43923264	1381	GGGCACCCTGG ACAAAGAAATTC CC[C/T]AAGCACC TTCCCCTCCATT CCCCAC	C	T			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2803	cg43923264	1693	TCAGGGAGGGA AGGGGAGCAGG CTG[gap/G]CCCC CAAGCCCTCCCA CGCAGAGGA	gap	G			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3

2804	cg43923264	304	AGGCGGGGCTACTACGGGGCGGTGC[C/gap]TGCTGTGGAAATGCCTGCCCGCGCG	C	gap			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2805	cg43916919	104	CTTTATTGAACATCTGCAGGGGGCA[C/gap]CTCTGCACTGACCAGGCAGCCAGAG	C	gap			SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.|pcls:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.	4.30E-188	2 (2cen)
2806	cg43949677	1733	CCTTTTGCTGGATATGCAGAAATGA[T/C]AGGAAAAAAACCAATGGTGAAATTT	T	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
2807	cg42894986	1436	ATTCCAGCTCCTGGCCCTCCTGGAA[C/G]CCAGGCTCTAAACAAGCAGGGAGAG	C	G			SILENT-NONCODING	struct	Human Gene SPTREMBL-ID:Q28686 50-KDA DYSTROPHIN-ASSOCIATED GLYCOPROTEIN PRECURSOR - ORYCTOLAGUS CUNICULUS (RABBIT), 387 aa.	1.40E-180	17
2808	cg43971282	606	ATGCTGGGGACACTACAGGCACACA[G/C]AGGAATAGCAGGGCCACCCTCAGAG	G	C			SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P97490 ADENYLATE CYCLASE, TYPE VIII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLYL CYCLASE) - MUS MUSCULUS (MOUSE), 1249 aa.	8.90E-180	2

2809	cg43962437	1425	AGGAGGACCTG GGGGGGGCAAG AGC[gap/C]TCAG GAGAAGGCGTG CCGCCCTTCC	gap	C		SILENT-NONCODING	struct	Human Gene SWISSNEW-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.|pcls:SWISSPROT-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.|pcls:TREMBLNEW-ID:G2707601 SYNAPTOPHYSIN - HOMO SAPIENS (HUMAN), 313 aa.	4.80E-173	X (Xp11.23)
2810	cg43956325	17	TCGTCTTTTTTTT TTT[A/T]CTTTTAA CAAAAGCAACAA TTTTTA	A	T		SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2811	cg43956325	239	TTATAGAACAAT GAAAATTCCTGT T[A/C]GGAACACA AGTTGCTGTTTA TATTT	A	C		SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2812	cg43956325	312	AGAAGAAGTAAG GTGGAGCTGTTG G[G/A]AAAGCCC ATCGTGGACCTT TGGAGA	G	A		SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)

2813	cg43956325	67	ATTATCTTGCTTTATATTTAATGGA[T/G]TAGAACTATAAAGATTCTTAACTTT	T	G		SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2814	cg43985529	126	ATGCAGGGGCGTGCATTGGCTGCTG[C/gap]CGCTTTTGTAATTGAATTGTTTTAA	C	gap		SILENT-NONCODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA-E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
2815	cg43985529	127	TGCAGGGGCGTGCATTGGCTGCTGC[C/gap]GCTTTTGTAATTGAATTGTTTTAA	C	gap		SILENT-NONCODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA-E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
2816	cg43305278	336	GGGGGAGCTTCTGGTCCTGGGGGTA[C/gap]CCACTTGTGAGGGAGTGGGGGACA	C	gap		SILENT-NONCODING	struct	Human Gene SWISSPROT-ID:P51911 CALPONIN H1, SMOOTH MUSCLE (BASIC CALPONIN) - HOMO SAPIENS (HUMAN), 297 aa.|pdb:SPTREMBL-ID:Q15416 BASIC CALPONIN - HOMO SAPIENS (HUMAN), 297 aa.	3.10E-162	19
2817	cg44017869	323	AAATGGGAACAAATATAGATAATCG[T/G]TTCCTGGGTCAAAGGCATTTAGAAA	T	G		SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:Q63537 SYNAPSIN 2A - RATTUS NORVEGICUS (RAT), 586 aa.	5.20E-148	
2818	cg42914441	116	CCAGACCGTTCCCGGGCCGGCCAGC[G/C]GCCACCATGGTGGCCCTGAGGCCTG	G	C		SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P26044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa.	5.40E-133	22 (22q12.2)

2819	cg43929931	1325	GCACCGCGTTTC CATAGCAGCATG T[C/gap]CTACGG AAACCCAGCACG TGTGTAG	C	gap		SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:Q64572 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) (PHOSPHORYLASE B KINASE KINASE) (GLYCOGEN SYNTHASE A KINASE) (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE) - RATTUS NORVEGICUS (RAT), 505 aa.	7.60E-132	12
2820	cg43929931	1326	CACCGCGTTTCC ATAGCAGCATGT C[C/gap]TACGGA AACCCAGCACGT GTGTAGA	C	gap		SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:Q64572 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) (PHOSPHORYLASE B KINASE KINASE) (GLYCOGEN SYNTHASE A KINASE) (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE) - RATTUS NORVEGICUS (RAT), 505 aa.	7.60E-132	12
2821	cg43918346	913	TTCTGAGTGCAT GAAGTTATAAAG G[A/T]CCTACATG TAATGCATATGT GATGC	A	T		SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2822	cg43918346	797	CAGCTTCTTTGT TAATACACCCAT G[G/C]TAAATTTC AACAGTGCCACA TCTGC	G	C		SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	

2823	cg43918346	848	ATTCTCTGTTCTCAAGGCACCTGGA[A/T]GGTGACCCGGGGCCGTCCTCTCCTC	A	T			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2824	cg43918346	857	TCTCAAGGCACCTGGAAGGTGACCC[G/T]GGGCCGTCCTCTCCTCCTCTTCATG	G	T			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2825	cg43942332	1232	GTGTTCGGTGGGAAGGTGGGATTTT[T/G]GGTTCTCTGGAATTGAATGTTTAGT	T	G			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2826	cg43942332	1542	AATAAGAAATTTTAATGCACGAGTA[A/G]AGGGGGTGGTGGGTTGTGCACTTTT	A	G			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2827	cg43942332	398	GCTATATAATTTTAATCTAAAGATT[T/G]GGGCATACAGAAAGCATTTCACATA	T	G			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2828	cg43942340	44	TTTTTTTTTTTTTTTTTTTTT[C/T]AAAAGGAAATCCCAATCTTTTTATT	C	T			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	1.20E-123	11

2829	cg43942338	1072	GTGTTCGGTGGGAAGGTGGGATTTT[T/G]GGTTCTCTGGAATTGAATGTTTAGT	T	G			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2830	cg43942338	1194	ACCCCACCGAGAAAAAAGAGCACCA[G/A]GAAAAGAGCAGAAGAGGACAAGAGA	G	A			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2831	cg43942338	1382	AATAAGAAATTTTAATGCACGAGTA[A/G]AGGGGGTGGTGGGTTGTGCACTTTT	A	G			SILENT-NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2832	cg43961212	882	TACCACGGGTCATTTAGAAAAACAG[A/gap]AAAAAAATATACACCTAGTCTTTGC	A	gap			SILENT-NONCODING	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
2833	cg43961212	889	GGTCATTTAGAAAAACAGAAAAAAA[A/gap]TATACACCTAGTCTTTGCAATTAAA	A	gap			SILENT-NONCODING	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
2834	cg43981852	150	CAGAGGTCGAGGAGCTCGCCTGGGC[G/gap]TAGACATCCTCCACAGGAACAGTGA	G	gap			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN-LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
2835	cg43981852	344	AGATGAAGGTGGCGTGTGGCTGTGG[C/gap]CCTACGCATCCCCGTTCTCCATGCG	C	gap			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN-LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	

2836	cg43981852	346	ATGAAGGTGGC GTGTGGCTGTG GCC[C/gap]TACG CATCCCCGTTCT CCATGCGGC	C	gap			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN-LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
2837	cg43051163	952	GGGATCTTTGGC AGAGGAGTGATC T[A/G]AGAAGAAA CCGAGAGACGT GGCGTC	A	G			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2838	cg43051163	292	TTAACTCACCCT GGTATGGCTAAA G[C/gap]CAAGGG CCAGGCACCTG GAAGACTC	C	gap			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2839	cg43051163	293	TAACTCACCCTG GTATGGCTAAAG C[C/gap]AAGGGC CAGGCACCTGG AAGACTCT	C	gap			SILENT-NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2840	cg42887734	977	GCTTCTATCCAC CCATGAGGCACC T[G/gap]GGGCTT CTCAGCCACCCC GTGGTGT	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94	1 (1q31.3)
2841	cg42887734	980	TCTATCCACCCA TGAGGCACCTG GG[G/gap]CTTCT CAGCCACCCCGT GGTGTAAC	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94	1 (1q31.3)
2842	cg42887734	866	CCCCACTTCTTC CCTCCAGCCTGC A[gap/A]TGCCCT CCTCTGGAACTG GGATTAA	gap	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94	1 (1q31.3)

2843	cg42893961	565	GAGAAAGAGGAA TGAGGGGCAGG GC[C/gap]AGGCC ACGGGGGGGCA CCTCAATAA	C	gap			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa.	2.50E-89	
2844	cg42896604	269	CCTTCATTTTTTT TTTTTTTTTTT[A /T]AGAAACAAAG ATCAGTTAAATTT TA	A	T			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q14843 MYOSIN LIGHT CHAIN 2 - HOMO SAPIENS (HUMAN), 170 aa.	8.60E-87	12 (12q23)
2845	cg43282400	2067	TAATGAAAATAAT TTGTAAAATGTC[C/gap]TTTAAAAG TTTAATGATACTT CTGA	C	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P45591 COFILIN, MUSCLE ISOFORM - MUS MUSCULUS (MOUSE), 166 aa.	8.00E-84	14
2846	cg43336710	150	CTTCTGTGCTGC ATGCAGAGGGG TG[C/T]AAGGCCA GGGCAGCTGAC CTGGTCA	C	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P13928 ANNEXIN VIII (VASCULAR ANTICOAGULANT-BETA) (VAC-BETA) - HOMO SAPIENS (HUMAN), 327 aa.	1.70E-83	10 (10q11.2)
2847	cg43336710	336	TCTCGGTTGGGA TGGATTCGTGTT C[G/A]TTTCTCAG CTGCTGAAGGAT GTGTG	G	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P13928 ANNEXIN VIII (VASCULAR ANTICOAGULANT-BETA) (VAC-BETA) - HOMO SAPIENS (HUMAN), 327 aa.	1.70E-83	10 (10q11.2)
2848	cg43135652	598	TCCTGGGGTTGG GGAGGGGGTCG GG[G/gap]TCCCA GGACCTGAGCCT GGCCATGT	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P02591 TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES (TN-C) - ORYCTOLAGUS CUNICULUS (RABBIT), 161 aa.	1.20E-82	3 (3p21.3)
2849	cg43976895	433	AGGGACGAGAG CCGTGGGTCCC AAC[G/gap]GGGG CCCTTGGACACC ACTGGCAAT	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P40145 ADENYLATE CYCLASE, TYPE VIII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLYL CYCLASE) - HOMO SAPIENS (HUMAN), 1251 aa.	9.40E-82	5

2850	cg43916621	564	AGCATTCCTGCTCCCCTCCGTGGGA[G/gap]CAGCGTCTCCTTTTCAATTCATGTG	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P35749 MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) - HOMO SAPIENS (HUMAN), 1086 aa (fragment).	2.80E-81	16 (16p13.13)
2851	cg42898003	312	CTTCCAGACAAAGACCCACAAGGGG[T/C]CGCGCCTCCCTGGTGGGGACCCGGC	T	C			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
2852	cg42898003	318	GACAAAGACCCACAAGGGGTCGCGC[C/gap]TCCCTGGTGGGGACCCGGCAGGGCG	C	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
2853	cg43919386	1505	ATACATATGGATGTTACTCTCTTGC[A/C]CCAAATTATCTTGATACATTCAAAT	A	C			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	9.80E-79	12 (12q21.3)
2854	cg43919386	1554	ATTTGTCTGGTTAAAAAATAGGTGG[T/A]AGATATTGAGGCCAAGAATATTGCA	T	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	9.80E-79	12 (12q21.3)
2855	cg42731508	1868	ACACCGGGTGACCCCTTAGGGCACC[C/gap]AGGCAAGATCCCTAAGAGGCACCCA	C	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2
2856	cg42731508	1986	CTCCCTCCGCGGTCGGATTCTGGAG[G/T]GTGGGAGGCATCTTGGCCTGCAGTA	G	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2

2857	cg44014373	205	GTGAGACTGTTA CAGAAAAAAAA A[T/gap]AAAAGTT TCTGAGTCTGAT AATTCC	T	gap			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.10E-70	17
2858	cg43977049	133	CTGGGGCCCGA GGAGCTCAGGA AAA[C/T]GGAAGC GGAGTCTTTGCA TAGTTCT	C	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:Q01995 SMOOTH MUSCLE PROTEIN 22-ALPHA (SM22-ALPHA) (TRANSGELIN) (WS3-10) (22 KD ACTIN-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 200 aa.	1.80E-69	
2859	cg42379998	254	ATCAAAACAAG TAAAGATGTTT A[T/C]AAAAGCCA TTTCCTTTTCTTT CCCC	T	C			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q63811 CALMODULIN-DEPENDENT PROTEIN PHOSPHATASE REGULATORY SUBUNIT BETA 2 ISOFORM - MUS MUSCULUS (MOUSE), 179 aa (fragment).	2.70E-67	
2860	cg43929049	1046	AGAAGTAAACCT CTAAAACTGAAG A[C/A]GACCCTCT AAAGGAGAAAAC TATAG	C	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2861	cg43929049	253	GGTTTCTATATA CCTTCTGGATTT T[A/gap]AAAAAAC CCAAAAATTAAT GGCTCA	A	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2862	cg43929049	259	ATATACCTTCTG GATTTTAAAAAAA [gap/A]CCCAAAA ATTAATGGCTCA AGATAC	gap	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2863	cg43929049	29	TTTTTTTTTTTT GTTTTAATTCAA TAAACATGTAGA TT	T	G			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2864	cg43929049	34	TTTTTTTTTTTTTTT /T]ATTCAATAAAC ATGTAGATTTATT T	A	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2865	cg43929049	35	TTTTTTTTTTTTTT /T]TTCAATAAACA TGTAGATTTATTT T	A	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2866	cg43929049	429	AAAATTACAGAA GCTTCAAATTGT T[A/G]TGTTTTCA CAAAATTTGCTA CATAT	A	G			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2867	cg43929049	737	AGGCACTTGAAA ACATTAAGTATAT [G/C]TACAAATGT GCAAGTAAAACA AACA	G	C			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2868	cg43929049	853	ATGCAGAGTTTG TTTATGAAATGA A[C/A]CAAAGCAG TTTGTCATTTCTT ACTA	C	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSNEW-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.|pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2869	cg43936426	358	GGGGAGGAGAG AGAAGGGGACA CCA[T/A]TTCTTT AGACACATCTGT GTTTCTG	T	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2870	cg43936426	430	GGCCAGGAGTTT GGGTGTGCACT GG[G/T]TGTCTTT CAACTGGGTGGA ACCAAA	G	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2871	cg43936426	450	ACTGGGTGTCTT TCAACTGGGTGG A[A/gap]CCAAAC TGAGTCCTTGAA GTCTCGC	A	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)

2872	cg43936426	480	ACTGAGTCCTTG AAGTCTCGCTCC T[G/T]AGGCTGCA GAAGAATAGATG GCTTT	G	T		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2873	cg43936426	493	AGTCTCGCTCCT GAGGCTGCAGA A[G/T]ATAGATG GCTTTTCCCTGC CTCGAG	A	T		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2874	cg43936426	520	TAGATGGCTTTT CCCTGCCTCGAG G[G/gap]TGGGAT AAGGGAGGCAA AGCTGGGA	G	gap		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2875	cg43936426	524	TGGCTTTTCCCT GCCTCGAGGGT GG[G/C]ATAAGG GAGGCAAAGCT GGGAGAAA	G	C		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2876	cg43936426	531	TCCCTGCCTCGA GGGTGGGATAA GG[G/gap]AGGCA AAGCTGGGAGAA AGAAAGGG	G	gap		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2877	cg43936426	553	AGGGAGGCAAA GCTGGGAGAAA GAA[A/G]GGGAG AGAGAGAAAACG AATGGCCG	A	G		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2878	cg43936426	587	GAGAAACGAAT GGCCGGCACAG GT[G/gap]CCTGG GCCCCAGCCTTC AAGTGCGG	G	gap		SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)

2879	cg43933305	418	ACAGTTAAGATA CATTAAAAAAAA A[A/gap]GGAAAG ATACCCACAATT CCATTCT	A	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2880	cg43933305	696	CACCTGTACAAC CTCCCCTGACAG A[T/C]AGTGAGAG CCGCGGCGGGG CCAGGG	T	C			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2881	cg43933305	740	GCCAGGGGCTC TGTGTGCTTTGG AG[G/gap]CTACT GCCTCTGGAATG TTTCGCAT	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2882	cg43986028	43	GGAGGCGCGAG TGAAGGAAGACG AA[G/gap]TGCGT GACCCGACCGG CTGTGGTGT	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:P91637 RIC (RAS WHICH INTERACTS WITH CALMODULIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 264 aa.	5.00E-59	1
2883	cg43986623	2964	CCATCGGTCCGT CCATCCATGTCC C[C/gap]AGTTGA CCGCCCGGCAC CACTAGCT	C	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P15941 MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN) (TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT-REACTIVE URINARY MUCIN) (PUM) - HOMO SAPIENS (HUMAN), 1255 aa.	6.60E-57	7 (7q11.23)
2884	cg43919048	1279	GAGGTGAGAGA ATTCCAAGTTTT GA[G/A]GGGAGT GGTCCAAAGAGT AACAACT	G	A			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q07569 MYOSIN HEAVY CHAIN - ENTAMOEBA HISTOLYTICA, 2139 aa.	1.70E-56	3

2885	cg43919048	186	GAGAGGCTAGGCAGTGAACACATCA[C/T]GTATGCAATGAGAAAATAACCAACT	C	T			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q07569 MYOSIN HEAVY CHAIN - ENTAMOEBA HISTOLYTICA, 2139 aa.	1.70E-56	3
2886	cg43927885	2154	ATGCTGGAGGTGGGGGTGCTGTGTT[C/T]TAGACCCCCCATATTATCCCAGTGT	C	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2887	cg43927885	641	CTCTCAGCCATATCTTTCAGCCCCC[C/A]CTCCCCTGGATCCGTGTGTGTGTGT	C	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2888	cg43927885	782	AGATGATTTTTCCGGTTGTCCTTAA[C/A]ACCCCTTCCTGAGGTTCCCTTCACC	C	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2889	cg43958532	254	TCCTGACTCCAGGCTAGGTCCCCAA[G/gap]GGGAGGTCAGGCTCAGACTTGGACC	G	gap			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20
2890	cg43958532	281	GGAGGTCAGGCTCAGACTTGGACCT[G/A]GGCGCTGGAAGTGTGAGTAATGGTT	G	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20

2891	cg43958532	69	TTTTCTTTTCAAG ATGCTACATAGT[C/G]AAACAGAAC TGGGTTGGTCTT TTAT	C	G			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20
2892	cg43977322	25	TTTTTTTTTTTTT TTTTTTTCAGA[C/ T]TCCAGCCACC AGGTTTATTTTCA TG	C	T			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2893	cg43977322	431	ATGGAAAGTTGG TTTTAAGCCAGA A[G/A]TCTGGAGA GATGTCATGCCA GGCAG	G	A			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2894	cg43977322	62	GGTTTATTTTCAT GCTATAAATAAA[T/G]TTCCCTATTA GTTCCCATTTTC TTA	T	G			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2895	cg43961860	215	AGTTTAGCAGTC TGCTTAAAATGT T[A/gap]AAAAAA AAATCATAAAAA GCCATT	A	gap			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.50E-51	
2896	cg43961860	225	TCTGCTTAAAAT GTTAAAAAAAAA A[A/gap]TCATAAA AAGCCATTGTTC TGTTAC	A	gap			SILENT-NONCODING	struct	Human Gene Similar to SPTREMBL-ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.50E-51	
2897	cg43918310	535	ATGCTGAATCCC CTATCCCATTCT G[T/C]GTATGAGT CCCATTTGCCTT GCAAT	T	C			SILENT-NONCODING	struct	Human Gene Similar to SWISSPROT-ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)

2898	cg42673122	249	ACCAGGAGGGGGCTGGGGGCGGCCA[G/gap]CACCAGCGGCGTCCTGCTCAGCCCC	G	gap			SILENT-NONCODING	sulfotransferase	Human Gene SPTREMBL-ID:Q99999 CEREBROSIDE SULFOTRANSFERASE HOMO SAPIENS (HUMAN), 423 aa.	1.50E-209	22
2899	cg43974392	1785	CCAGAGGGTGGTGTGGTGTCCAGGG[G/A]TCCATCTTTCCAGAATCCATGCCTG	G	A			SILENT-NONCODING	sulfotransferase	Human Gene TREMBLNEW-ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2900	cg43974392	2178	GATTCCTTTCATCTCAGCAAAATGG[G/gap]CACTGCCAGAGCCATTTCTGATCAC	G	gap			SILENT-NONCODING	sulfotransferase	Human Gene TREMBLNEW-ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2901	cg43974392	2311	AGTGCGGCTTCCTGGCAACAAGGTA[G/gap]GCCCTGGTGCAGGGCAAGCCGCAGC	G	gap			SILENT-NONCODING	sulfotransferase	Human Gene TREMBLNEW-ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2902	cg43999676	1452	AAAATTAGCCAGGAGCATTGGCTCA[G/gap]TGTCTGTAATCCCAGCACTTTGGGA	G	gap			SILENT-NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2903	cg43999676	1592	AAATTAGCCGGGCATGGTGGTGCAC[A/G]CCTATAGTCCCAGCTACTCGGGAGG	A	G			SILENT-NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)

2904	cg43999676	1615	ACACCTATAGTCCCAGCTACTCGGG[A/G]GGCTGAGGTAGGAGAATCGTTTGAA	A	G			SILENT-NONCODING.	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2905	cg43999676	1738	TCTCAAAAAGAAAGAAGTGACTAGG[G/gap]TTCAGAGAACCAGGGTTCAAAGCCC	G	gap			SILENT-NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2906	cg43317375	751	CACTAGGTCTTCAGAATGGACGTCC[T/C]TCTGCCAGAGACTTCCAGCGGGCGG	T	C			SILENT-NONCODING	sulfotransferase	Human Gene Homologous to TREMBLNEW-ID:E1253895 DJ388M5.3 (SULFOTRANSFERASE (SULFOKINASE, EC 2.8.2.1) LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 284 aa.	8.50E-133	22
2907	cg43972499	141	AATGAAGATGGGGCAGACTGGGCCC[C/gap]AGCATCTGAGGCCCCACCCCCATGC	C	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0.00E+00	2

2908	cg43972499	50	TTTTTTTTTTTTT[T/A]TCAAGGGACA GCTCGGCTGTTT ATT	T	A			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0.00E+00	2
2909	cg43986130	186	CGCACACAATAA GCTGGGCCTGA GC[C/gap]AGGAG GCAGGCGGGGT GTTGGGGGA	C	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2910	cg43986130	279	GGGAGCCCCTC TGCTATCTCAGC CA[A/G]GAGGAA GGAGAGACCAA GGCACAGA	A	G			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2911	cg43986130	47	AAACAAAGGCT TTAATTCACTCC A[G/A]CCACCCTC TGTCCCGCAGTG TCCCA	G	A			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2912	cg43986130	83	TCCCGCAGTGTC CCAGGCAGAGG CC[C/gap]TCTCC CTTCCCAGAAGG CACTGGGA	C	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9

2913	cg43054994	2317	CATGGTGAATAT AAGAACTGAATT C[T/gap]ACATGT GCTGCATGAAGA GCTAATT	T	gap			SILENT-NONCODING	synthase	Human Gene SWISSNEW-ID:P54840 GLYCOGEN [STARCH] SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.|pcls:SWISSPROT-ID:P54840 GLYCOGEN (STARCH) SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.|pcls:TREMBLNEW-ID:E1228798 LIVER GLYCOGEN SYNTHASE - HOMO SAPIENS (HUMAN), 703 aa.	0.00E+00		12
2914	cg43054994	2820	AGAACCATGATT TAGATGTAGTTT T[A/G]CAGAGACA AAAATCCATGAG TGAAT	A	G			SILENT-NONCODING	synthase	Human Gene SWISSNEW-ID:P54840 GLYCOGEN [STARCH] SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.|pcls:SWISSPROT-ID:P54840 GLYCOGEN (STARCH) SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.|pcls:TREMBLNEW-ID:E1228798 LIVER GLYCOGEN SYNTHASE - HOMO SAPIENS (HUMAN), 703 aa.	0.00E+00		12
2915	cg40388639	5040	GCCGGCTGCAA GTTTGTAAGCGC GG[G/gap]ACAGA CACTGCTGAACC TTTCCTCT	G	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0.00E+00	(12q24.2)	12
2916	cg43987111	680	TTGAGAAACAAG GTGACCGATGG GG[C/gap]ACTCT GCAGCCCCACC CACCATCGG	C	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	(1p34.1)	18
2917	cg43981333	18	TTTTTTTTTAGCT ATCC[G/A]ATAAT TATTTATTGAAAG AAATGAC	G	A			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P18858 DNA LIGASE I (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) - HOMO SAPIENS (HUMAN), 919 aa.	0.00E+00	(19q13.2)	19

2918	cg43971304	2483	CCCCGATCCAGA TCTGCACGGGGT G[T/C]GGCCCCCG CAGTGCCCCCAC CCAGTC	T			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2919	cg43971304	2559	TCCAGTTTCCAA GTTCCTGCACTC C[A/T]GAATCCAC AAAGCCGTGCCT TTCTC	A	T		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2920	cg43971304	2654	TGGACCGCTTCC CAGAGGCCAGG AA[gap/A]TCTGC CATTACTCTGCG GTGGTGCC	gap	A		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2921	cg43971304	2953	GAGGGATGTTCT AGCCCTCCCTGG C[A/gap]TGTCAG AGCCAGGCTCTG CCTGGAG	A	gap		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2922	cg43971304	68	GAGCGTCTTGCA AGCTTCCCGTCG G[G/gap]CACCAG CTACTCGGCCCC GCACCCT	G	gap		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2923	cg43918681	33	TTTTTTTTTCACC ATTTTTTTTTTT[T /A]TTTATTTCCAG GACTATGTTTTTA C	T	A		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P13196 5-AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA-AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0.00E+00	3 (3p21.1)

2924	cg43983214	494	GACCCAAGTGAAGCGCAGGTGGGGT[G/T]TGAATCCTAGGCAGCTGGCTTCTCA	G	T		SILENT-NONCODING	synthase	Human Gene SPTREMBL-ID:Q13735 5-AMINOLEVULINATE SYNTHASE PRECURSOR - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	X (Xp11.21)
2925	cg43949316	211	TTATTTAAAACAGGGATCCATCAGA[G/C]GTGGTGAACTATCAAGGTCAAGGTT	G	C		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2926	cg43949316	348	GAACAAACCCGATGTAAAAGGCACC[T/A]AGCTGGGGAGAAGCTGTGGTGTTCA	T	A		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2927	cg43949316	591	TTCTGCTCTAGAAGGAAGGGGAACC[C/gap]TTCCCCCAGTATCAATTTCAGCAGC	C	gap		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2928	cg43967343	384	CCCCGCGTGCAGAACCCTGCTTGCA[G/gap]CTCAGGTTTCGGGGTGCTTGAGGAG	G	gap		SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:Q92903 PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) - HOMO SAPIENS (HUMAN), 461 aa.|pdb:SPTREMBL-ID:O00163 CDP-DIACYLGLYCEROL SYNTHASE - HOMO SAPIENS (HUMAN), 461 aa.	8.50E-254	4

2929	cg43976335	108	AAGGCAGAATTAGGGAAAGGCTATG[C/gap]CCCTCCACTCCCCCTCCTCCTACCA	C	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2930	cg43976335	111	GCAGAATTAGGGAAAGGCTATGCCC[C/gap]TCCACTCCCCCTCCTCCTACCACTC	C	gap			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2931	cg43976335	182	ACTGGAACCTGCTGAAAAGGCTGAT[G/A]AGGGGCTGACAGGAGTGGGGCAGGG	G	A			SILENT-NONCODING	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2932	cg43959826	522	GCCGATGCCTGGCTCCATCCAGAGC[C/gap]AGCCCAGCCCAGGGAGGCTGCATGG	C	gap			SILENT-NONCODING	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN- III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7.00E-140	10 (10q25.2)
2933	cg43953338	2968	TTTGTGTTTTCATCTCCTAAAAGTG[T/G]TTTTTATTTCCTTGTATCTGTAGTC	T	G			SILENT-NONCODING	synthase	Human Gene Homologous to SWISSPROT-ID:P44708 GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa.	3.10E-107	2 (2p13)

2934	cg43982623	106	TCCTGCCTCCTC TCTCAGACAGGG A[G/A]GCGGGAA CCAGACTTACTG ATCCAA	G	A			SILENT-NONCODING	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS TAURUS (BOVINE), 402 aa.	8.20E-105	1
2935	cg43982623	200	GCAGCGACACA GCATCCCCTCTG GT[C/gap]CCCTC CTGGGGCTGCT CCTCAGCAG	C	gap			SILENT-NONCODING	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS TAURUS (BOVINE), 402 aa.	8.20E-105	1
2936	cg43982623	211	GCATCCCCTCTG GTCCCCTCCTGG G[G/gap]CTGCTC CTCAGCAGGGG GCGCACCA	G	gap			SILENT-NONCODING	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS TAURUS (BOVINE), 402 aa.	8.20E-105	1
2937	cg43987048	35	TTTTTTTTTTTT TTTTTTTTTTA[A /G]CATTTAAAAAT CAGTATTTAATTA C	A	G			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:G2984031 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II - AQUIFEX AEOLICUS, 415 aa.	1.20E-86	

2938	cg43124627	1928	TTTCATTAATTAC CATATCTATAAA[A/gap]CAAACATA GTATCTGTCAAT CTCTA	A	gap			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16
2939	cg43933068	289	AGCCAGGGTCG GTGAAGGATCCC AA[A/G]ATGGCTG GGCGAAAACTTG CTCTAA	A	G			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.90E-75	12
2940	cg43275028	3001	ACACCTAAGCCA AGACACTGGTTC T[C/gap]CTTCCG GAATGAGGCCCT GGGAGGA	C	gap			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O-ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.|pcls:SPTREMBL-ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2941	cg43275028	3213	ATGAAGACACAG CTGTTAACAATT G[G/gap]CTGATC AGCCCCCAGAAT GCCTCAC	G	gap			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O-ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.|pcls:SPTREMBL-ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

2942	cg43275028	705	CTTACCTTGACC ACACATTCCCTG C[G/A]GAGAAGA TGGACGACGCT GTGGCTC	G	A			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O-ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.|pcls:SPTREMBL-ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2943	cg43275028	7134	ATTTTATACAAGA AGATAAAAAAAT[A/G]TAACTCCTT GCTACCAGTAAG TAAG	A	G			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O-ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.|pcls:SPTREMBL-ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2944	cg43275028	852	AAAATCTGATCG AGGATTTCAACT C[G/T]GGGCTGA TTGGGCCCCTGC TTATCT	G	T			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O-ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.|pcls:SPTREMBL-ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.2E-65	1 (1q23)
2945	cg42521802	1609	AGTCTCCAGAAC CCATGATGAACT G[T/gap]GATCTG CCGTGGTCCTGC CGTGGTC	T	gap			SILENT-NONCODING	synthase	Human Gene Similar to SWISSPROT-ID:P15535 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - MUS MUSCULUS (MOUSE), 399 aa.	3.7E-65	

2946	cg43064068	1672	TCCGGAAAAGCCCGTGCGCAGTGAG[A/G]CATCTAAGAGACATTCATTTGGATT	A	G			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
2947	cg43064068	1674	CGGAAAAGCCCGTGCGCAGTGAGAC[A/G]TCTAAGAGACATTCATTTGGATTCC	A	G			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
2948	cg43064068	1679	AAGCCCGTGCGCAGTGAGACATCTA[A/G]GAGACATTCATTTGGATTCCCCTCT	A	G			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	

2949	cg43064068	1741	CTTTTCCCTTTG GGCCCTTGGCCT T[C/A]CTATGATG ATATGAGATTCT TTATG	C	A			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
2950	cg43064068	1767	CTATGATGATAT GAGATTCTTTAT G[G/A]AAGAACAT GAATATAAGTTTT GTCT	G	A			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
2951	cg43064068	1780	AGATTCTTTATG GAAGAACATGAA T[A/G]TAAGTTTT GTCTTGCCCTGG TTTTG	A	G			SILENT-NONCODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	

2952	cg42875572	162	GCAGTTTTTTAC TATTTACAAAATG [T/C]CATTTAGAG TGGAGGTGGCC ACCTT	T	C			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2953	cg42875572	168	TTTTACTATTTAC AAAATGTCATTT[A/G]GAGTGGAG GTGGCCACCTTC AGTAG	A	G			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2954	cg42875572	174	TATTTACAAAATG TCATTTAGAGTG[G/A]AGGTGGCCA CCTTCAGTAGCT GAGG	G	A			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2955	cg42875572	213	CAGTAGCTGAGG CAATGTCTTTCA C[G/A]TGAGATG GCCACAGAAGTG TGGTTC	G	A			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2956	cg42875572	226	AATGTCTTTCAC GTGAGATGGCCA C[A/T]GAAGTGTG GTTCCTGGAACT GGCTC	A	T			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2957	cg42875572	245	GGCCACAGAAGT GTGGTTCCTGGA A[C/T]TGGCTCAC AAAGGCCACAG GCTGTC	C	T			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2958	cg42875572	253	AAGTGTGGTTCC TGGAACTGGCTC A[C/G]AAAGGCC ACAGGCTGTCCT GGGTGA	C	G			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14

2959	cg42875572	324	GCACCAAAAAGG CTCAGTCTTCTG T[T/C]TCTTCATA CGTCGTCTCGTC AAAGG	T	C			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.80E-53	14
2960	cg42875572	333	AGGCTCAGTCTT CTGTTTCTTCATA [C/G]GTCGTCTC GTCAAAGGGCCT GTCCA	C	G			SILENT-NONCODING	synthase	Human Gene Similar to TREMBLNEW-ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.80E-53	14
2961	cg43931248	2107	CATGGGGGCTG TATTTAAGGACA CC[C/gap]GTGCC CCAAGCCCACCT GGGGCCCC	C	gap			SILENT-NONCODING	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
2962	cg43931248	713	ACCACTGCGCCC TTCTCCCTGAGG A[gap/G]CCTCAG CTTTCCCTCGAG GCCCTCC	gap	G			SILENT-NONCODING	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
2963	cg43274187	57	TGAGTATCTACA TTCAATTGCTTTA [G/gap]CTAAATTA ACAAAAAACATG CAAAT	G	gap			SILENT-NONCODING	tgf	Human Gene SWISSPROT-ID:O00292 TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR) - HOMO SAPIENS (HUMAN), 370 aa.	1.4E-186	
2964	cg43980446	1401	GTCCATCAATTG AAAGCACATTCC C[A/G]TACGTTTG CTGGAAGGATG GCATGT	A	G			SILENT-NONCODING	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN-2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2965	cg43980446	1658	TGATGATTCTGA TTGGGGGAAAAT A[T/C]AGTTCTAC CTATCTATATTTG TTTT	T	C			SILENT-NONCODING	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN-2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)

2966	cg43980446	1701	TTTGTTTTTCTTTTAATTATTTGGT[C/T]TCTGGATGGTGAATTAATGAAGCAA	C	T			SILENT-NONCODING	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN-2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2967	cg43980446	795	ATCCATGCAAGAACACAAAGCCTAT[T/G]TTAAACTAAAAAAAAAGAAGAGATT	T	G			SILENT-NONCODING	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN-2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2968	cg43980446	796	TCCATGCAAGAACACAAAGCCTAT[T/G]TTAAACTAAAAAAAAAGAAGAGATTG	T	G			SILENT-NONCODING	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN-2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2969	cg43980446	797	CCATGCAAGAACACAAAGCCTATT[T/G]TAAACTAAAAAAAAAGAAGAGATTGT	T	G			SILENT-NONCODING	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN-2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2970	cg43332146	777	TCAAAACTCTGTCAAGAACTCCGTC[T/G]GCTTGGGGTTATTCAGTGTGACCTA	T	G			SILENT-NONCODING	tgf	Human Gene Similar to SWISSPROT-ID:P01135 TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF) (ETGF) (TGF TYPE 1) - HOMO SAPIENS (HUMAN), 160 aa.	5.2E-84	2 (2p13)
2971	cg43047272	1700	GGCGGCCTAGGGGAAGATCGGGGAG[gap/G]CTGGTTTTGATGAAAGTATGTTAAC	gap	G			SILENT-NONCODING	tgf	Human Gene Similar to SPTREMBL-ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	5.2E-74	
2972	cg43047272	1740	GTATGTTAACTTTTCTTTTCCACTT[gap/G]GGGACCCTGTTCAGTATCTTTTGTA	gap	G			SILENT-NONCODING	tgf	Human Gene Similar to SPTREMBL-ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	5.2E-74	

2973	cg43272560	3230	CCCAGCCCAGCTCAGCTCAGCTACT[G/gap]CCAAGGGCAGGACCAATGGCTGAGC	G	gap			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2974	cg43272560	3459	GCCCCTCACAGGCTTGGGGGTTTTC[A/T]ATGTGAAACACATGCCAGTTTTTAA	A	T			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2975	cg43272560	3700	AATTTGCACCTTTGTCTGGATGCAC[A/T]CTTCTGACCTTGCTGCCACAACCTG	A	T			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2976	cg43272560	3744	CAACCTGTGGGGTCTGATGTGTCCC[T/A]TGATGGGTGCTGCCCTCAGGGACTG	T	A			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2977	cg43272560	3745	AACCTGTGGGGTCTGATGTGTCCCT[T/A]GATGGGTGCTGCCCTCAGGGACTGC	T	A			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2978	cg43272560	4243	TAGGCCCTTTCATAAAAACCAAACT[C/G]TAGCAAGATGCAAATGCATGGCAAA	C	G			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2979	cg43272560	4338	ACCAAGACAGTGCTGAGATTGGAAA[A/gap]GGGCACTCATTTGGATTGCCTTACT	A	gap			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)

2980	cg43261247	3334	CCCTAAACACTACCAAATAGCTCTT[A/C]TGGGGCAGGCTGGGCATGTCCAAAG	A	C			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:P37173 TGF-BETA RECEPTOR TYPE II PRECURSOR (TGFR-2) - HOMO SAPIENS (HUMAN), 567 aa.	2.0e-316	3 (3p22)
2981	cg43982633	458	CAGATACTATATTTGGATGTGACAG[G/T]TGTTTTTTCTTTTGTACAAGAGTGC	G	T			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2982	cg43982633	459	AGATACTATATTTGGATGTGACAGG[T/G]GTTTTTCTTTTGTACAAGAGTGCA	T	G			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2983	cg43982633	742	GAAGTAAAACTGTTAAAATCATCAT[C/gap]ATGATCATGATGATCATCATCATGA	C	gap			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2984	cg43982633	943	GCTTTCTTAAAAGGAAAAAAAAAAA[A/gap]TGTTCCAGTTGAATGGAACTGTTTC	A	gap			SILENT-NONCODING	tgfreceptor	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2985	cg43921327	1385	CCATGGACTCTTGCCTCGGTGCAGT[C/T]TCCACTCTTGACCCCCACCTCCTAC	C	T			SILENT-NONCODING	thioesterase	Human Gene Homologous to TREMBLNEW-ID:G2501961 PALMITOYL-PROTEIN THIOESTERASE 2 - HOMO SAPIENS (HUMAN), 302 aa.	1.1E-141	

2986	cg43918322	1109	CACAGCCCTGCCCATCTTCTGGGGC[C/gap]TGCGGGGACGACATCTAGTTCAATG	C	gap			SILENT-NONCODING	thioesterase	Human Gene Similar to SPTREMBL-ID:Q19781 SIMILAR TO ACYL-COA THIOESTERASE. NCBI GI: 1213545 - CAENORHABDITIS ELEGANS, 343 aa.	1.1E-53	20
2987	cg36988276	172	TGGAGGTTTTTCTCTGCAAATGCAG[G/A]AAGAAATCAGGTGGATGGATGCATA	G	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
2988	cg44030467	1747	TTCTCAAACGGTACACAGACTATTG[A/G]CATCAGCATCACCTAGAAACTTGTT	A	G			SILENT-NONCODING	tm7	Human Gene TREMBLNEW-ID:E1248507 C3A ANAPHYLATOXIN RECEPTOR - HOMO SAPIENS (HUMAN), 482 aa.	3.9E-265	12
2989	cg43338230	264	GGGCTGCGGCAAGGGAGGGTGATGC[A/T]ATGTGGTCTGAAGCCCTGGAAGGGC	A	T			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P11229 MUSCARINIC ACETYLCHOLINE RECEPTOR M1 - HOMO SAPIENS (HUMAN), 460 aa.	7.7E-253	
2990	cg43946035	1974	GGGACTCTGATATAAAGGAAGAATA[A/gap]GTCACTGTAAAACAGAACTTTTAAA	A	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P24530 ENDOTHELIN B RECEPTOR PRECURSOR (ET-B) (ENDOTHELIN RECEPTOR NON-SELECTIVE TYPE) - HOMO SAPIENS (HUMAN), 442 aa.	1.1E-242	13 (13q22)
2991	cg41084924	1896	GGCATGGTACCAGCCCTGGGGCTGG[G/gap]CCCCCAGCTCAGGGGCAGCTCATA	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.7E-241	11
2992	cg43985000	1935	AGAAATGCTTTCCAAAACCGCAAGG[G/gap]TAGACTGGTTTATCCACCCACAACA	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4

2993	cg43985000	2222	TTCTACTTTTTTT AAGTGATTTTTT[T/gap]GTCCTTCA GCCAAACACAAT ATGGG	T	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2994	cg43985000	2252	TTCAGCCAAACA CAATATGGGCTC A[A/G]GTCACTTT TATTTGAAATGT CATTT	A	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2995	cg43985000	2787	AAAGATCGAATT TTTCAGATGATT C[G/A]GAAATTTT CATTCAGGTATT TGTAA	G	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2996	cg43985000	2863	ATCACCTCCTAT TCTCTTAATTTTT [G/C]TTAAAATGT TAACTGGCAGTA AGTC	G	C			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2997	cg43985000	2988	AATAATTACCCA CAAATGCCACCA G[gap/T]AACTTA CGATTCTTCACT TCTTGGG	gap	T			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2998	cg43985000	2994	TACCCACAAATG CCACCAGAACTT A[gap/A]CGATTC TTCACTTCTTGG GGTTTTC	gap	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
2999	cg43985000	3324	GTTGTGCCAAAG TGCATAGTCTGA G[gap/C]TAAAAT CTAGGTGATTGT TCATCAT	gap	C			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4

3000	cg43985000	4080	AGCCAGAAGCCA AGGCCCTGAGTT G[G/gap]CAGTGG CCCATAAGTGTA AAATAAA	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
3001	cg39565524	1715	CTAGCCTCAGCC GCTCCTGGTGG GG[gap/G]AATGG CTGGGGCTGGG CAGGACCCT	gap	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
3002	cg39565524	1727	CGCTCCTGGTG GGGAATGGCTG GGG[C/G]TGGGC AGGACCCTCCCA CACACCTG	C	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
3003	cg36847035	217	GTGCTCCTGGCT ACCTCGCACAGC G[G/gap]TGCCCG CCCGGCCGTCA GTACCATG	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P35372 MU-TYPE OPIOID RECEPTOR (MOR-1) HOMO SAPIENS (HUMAN), 400 aa.	1.40E-219	6 (6q24)
3004	cg42704619	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCAGC CGCGGTAAAC	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3005	cg42704619	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCCCTCCCG CTGCGGCTC	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

3006	cg42704619	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C/gap]TGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3007	cg42704619	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3008	cg43306266	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCAGC CGCGGTAAAC	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3009	cg43306266	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCCCTCCCG CTGCGGCTC	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3010	cg43306266	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C/gap]TGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3011	cg43306266	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

3012	cg44031327	952	CTCCTAAAGCAC GGACCAGCCGTT G[G/gap]AGCCCC CAAATCCAGTAG GGGGTGG	G	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P35414 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ - HOMO SAPIENS (HUMAN), 380 aa.	5.70E-209	11
3013	cg43263108	1724	CCAAGCCACTCC AAGAGCCAGCC CC[gap/C]TTTCT GCTCCACAAAAA CCACAGTT	gap	C			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR) - HOMO SAPIENS (HUMAN), 386 aa.	8.30E-208	19 (19q13.3)
3014	cg43282263	1976	CTGGAGGCTCC CATGGGCTAGGA GC[C/gap]AGTGT GAGGCTGTAACT TATACTAA	C	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P41231 P2U PURINOCEPTOR 1 (ATP RECEPTOR) (P2U1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 377 aa.	9.90E-205	
3015	cg43329467	2631	CCAGGACAATGA AATACTCCAGCA C[G/C]TGTGGCT GACGAATTTGTT TCTACA	G	C			SILENT-NONCODING	tm7	Human Gene SWISSNEW-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) - HOMO SAPIENS (HUMAN), 375 aa.|pcls:SWISSPROT-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) - HOMO SAPIENS (HUMAN), 375 aa.|pcls:TREMBLNEW-ID:G2656121 G-PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7

3016	cg4329467	680	CTTTCGGCAAATCTTGAAAGCTGCA[G/C]GGCGCAGAGACATGGATGTGACTTC	G	C			SILENT-NONCODING	tm7	Human Gene SWISSNEW-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) - HOMO SAPIENS (HUMAN), 375 aa.|pcls:SWISSPROT-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) - HOMO SAPIENS (HUMAN), 375 aa.|pcls:TREMBLNEW-ID:G2656121 G-PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7
3017	cg38277960	1396	AGCTACCTCAACCAATGCCGAAAAA[gap/A]GACAGGGCTGATAAGCTAACACCAG	gap	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P32248 C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7) (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1) (EBI1) (BLR2) - HOMO SAPIENS (HUMAN), 378 aa.	4.10E-199	17 (17q12)
3018	cg2751286	1554	TTTGTGTCTTAAACGTGAGAGCAAA[gap/A]TGCATGTAATCCAACATGGCTACTT	gap	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3019	cg2751286	1566	AACGTGAGAGCAAATGCATGTAATC[C/gap]AACATGGCTACTTGCTTTGAAGGCT	C	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X

3020	cg2751286	1587	AATCCAACATGGCTACTTGCTTTGA[A/gap]GGCTCACCAGAATTATTTTTAAGTG	A	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3021	cg2751286	1601	ACTTGCTTTGAAGGCTCACCAGAAT[T/gap]ATTTTTAAGTGGTTTTAATAAAATA	T	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3022	cg2751286	1607	TTTGAAGGCTCACCAGAATTATTTT[T/gap]AAGTGGTTTTAATAAAATAACAAAT	T	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3023	cg2751286	1616	TCACCAGAATTATTTTTAAGTGGTT[T/A]TAATAAAATAACAAATTTTGACCTA	T	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3024	cg2751286	414	TAAGAGTTCTATGTTTTTCTCACAG[gap/G]AAGGCATAAGAACTAGGAGCTGCTG	gap	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3025	cg43031008	540	CTTTCTAGCCATTTGTTGGCAAGAA[A/gap]TAATAATTAAATTTTTTATTAAAAC	A	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3026	cg43031008	551	TTTGTTGGCAAGAAATAATAATTAA[A/gap]TTTTTTATTAAAACAAAACTTTTA	A	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)

3027	cg43031008	635	TATTCGTTTACAAATAAAAATGAAA[gap/A]TATTTATTTGCATTTTTATTGTGCT	gap	A			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3028	cg43031008	720	TACTTCCGAGTTGGAGATGGGAAAG[T/C]GCCCAATGAAAGAAATATAAAAGAA	T	C			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3029	cg42704646	117	GCGGCTGCGCCCCGCACCATGGGGG[gap/G]CAGCCCAGCCCCAGCCGCGGTAAAC	gap	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3030	cg42704646	167	GCCGACCTCCGCCGCCGCCCGCGCC[gap/G]CGTCTGCCCCCTCCCGCTGCGGCTC	gap	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3031	cg42704646	52	TGGCTCCCTCCCGGGCCAGTGAGCC[gap/C]TGGCGCCGCCGCGGCCGCGTCCCAG	gap	C			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3032	cg42704646	71	TGAGCCTGGCGCCGCCGCGGCCGCG[gap/G]TCCCAGCAGCGGAGTAGGGCGGCGG	gap	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)

3033	cg43308845	1524	AGTGAGGGGAA ACCAGGGCCTG AGC[C/gap]AAGC TAGAATTCCCTC TCTCTGACT	C	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P49238 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMKBRL-1) (CMKBLR1) - HOMO SAPIENS (HUMAN), 355 aa.	2.00E-190	3 (14q11.2)
3034	cg43308845	2647	CCCCCCTAGAAA CGTTTGGAACAA T[C/G]TAAAACTT TAAAGCTCGAAA ACAAT	C	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P49238 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMKBRL-1) (CMKBLR1) - HOMO SAPIENS (HUMAN), 355 aa.	2.00E-190	3 (14q11.2)
3035	cg43047341	671	GAAGGCAGGCC CAGGCTGTGACA GC[C/gap]GCCAG TATCCAGCAGCA CGCCCAGG	C	gap			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR) - HOMO SAPIENS (HUMAN), 369 aa.	2.80E-190	
3036	cg43328050	1796	GCGGACGTCAG CACTCACGGCCT GC[A/G]GGGACT CAGCACAGCTCT GGATTCT	A	G			SILENT-NONCODING	tm7	Human Gene TREMBLNEW-ID:E322207 P2Y-LIKE G-PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 367 aa.	3.30E-188	2
3037	cg42268169	7500	CACTTGAGCCCA GGAGTTTGAGAC T[A/G]CAGTGAAC TATGATTGCACC ACTGC	A	G			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P56486 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 343 aa.	4.90E-177	
3038	cg42268169	7533	CTATGATTGCAC CACTGCACTCCA G[A/C]CTAGGTG ACAGAGTAAGAC CCTGAC	A	C			SILENT-NONCODING	tm7	Human Gene SWISSPROT-ID:P56486 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 343 aa.	4.90E-177	

3039	cg44011188	1412	AGCTGAGCTGAC CCCAAGCCGAA GG[gap/G]TCCCG ACTCCTCTCGGG AGCCTGGA	gap	G			SILENT-NONCODING	tm7	Human Gene Homologous to SWISSPROT-ID:P35626 BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (BETA-ARK-2) (G-PROTEIN COUPLED RECEPTOR KINASE 3) - HOMO SAPIENS (HUMAN), 688 aa.	3.10E-119	22
3040	cg43993798	131	ATCCACATAAGA GCTCTGAGGGG AA[G/A]GAATGAT TATTATCCTTATT TTAAA	G	A			SILENT-NONCODING	tm7	Human Gene Homologous to SWISSPROT-ID:P31421 METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR - RATTUS NORVEGICUS (RAT), 872 aa.	6.90E-109	3 (3q21)
3041	cg42891000	1295	TGAGTCCAAGCC CTTCTCTGGTAC A[C/gap]TTAGTC CCAGTCTCTGGA ATATTTG	C	gap			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3042	cg42891000	1606	TGGAGGGAGAT GTGGAGCTGAC CCT[G/C]TCCAG CCTGTCCACGGA GAGGAAGG	G	C			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3043	cg42891000	530	AGCAGGCCTTAT TATTATTATTATT[T/A]TTTTTTTTG CTGACAAGTCCA AGA	T	A			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3044	cg42891000	649	CCTGCTTCCTTT TGCCTGTTATTA A[T/C]CGCTGCAA TAAAGCCATTAG AATCT	T	C			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3045	cg42891000	973	CCCCAGGATTCC AAGAGCCCAAAT C[C/gap]TGCGGT GGGAGTGAAGG GGAGGCAG	C	gap			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)

3046	cg43285474	2177	TGGTTGAATGATTTCCCACTCAGGG[C/gap]CTGGGGCCAAGAGGAAAAACAGGGA	C	gap			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P30083 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP-R-2) - RATTUS NORVEGICUS (RAT), 459 aa.	4.40E-85	3 (3p22)
3047	cg42284367	1202	TTTTCCAGCAAGAGGCTCCCGAGCG[A/G]GCAAGCTCAGTTTACACCCGATCCA	A	G			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.80E-83	3 (3q21)
3048	cg42284367	1216	GCTCCCGAGCGAGCAAGCTCAGTTT[A/T]CACCCGATCCACTGGGGAGCAGGAA	A	T			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.80E-83	3 (3q21)
3049	cg11687629	323	TCAGCTTCCAGTCTTATCTGAAGAC[C/T]CCGGCACCAAAGTGACCAGGAGGCA	C	T			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	8.90E-83	
3050	cg43970708	258	TCAGCTCACTGCAGCCTCCACCTCC[C/T]GGGTTCAAGCGATTCTCCTGCCTCA	C	T			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3051	cg43970708	262	CTCACTGCAGCCTCCACCTCCCGGG[T/C]TCAAGCGATTCTCCTGCCTCAGCCT	T	C			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3052	cg43970708	277	ACCTCCCGGGTTCAAGCGATTCTCC[T/C]GCCTCAGCCTCCCAAGTAGCTGGGA	T	C			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	

3053	cg43970708	324	GGGACTACAGG CGCATGCCACCA TG[C/T]CTGGCTA ATTTTTGTATTTT TAGTA	C	T			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3054	cg43089531	408	TTTAAAAGCTTT GATTAGAAGCCA A[C/T]TTGATTTA GGAGTTCCCACT GGCAA	C	T			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3055	cg43089531	435	TGATTTAGGAGT TCCCACTGGCAA A[A/T]TAGGGAAC AATATGAGCATC AAGGA	A	T			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3056	cg43089531	803	AGCATTTTCACG TTTGACATGATA G[T/C]AACTCAAA CTAACTCTTTAC CACAT	T	C			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3057	cg21411454	1822	AATGTGCTCTCC TAGGCCACAGG GC[C/gap]TTTGG CAGGTGCAGCC CCCACTGCC	C	gap			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3058	cg21411454	466	CAGCTTTCAAAA AGAGTGCTGCCC A[G/T]AAAAAGCC TTCCACCCTCCT GTCTG	G	T			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3059	cg21411454	492	AAAAAGCCTTCC ACCCTCCTGTCT G[G/gap]CTTTAG AAGGACCCTGAG CCCCAGG	G	gap			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2

3060	cg21411454	523	GAAGGACCCTGA GCCCCAGGCGC CA[G/gap]CCACA GGACTCTGCTGC AGAGGGGG	G	gap			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3061	cg21411454	563	GCAGAGGGGGG TTGTGTACAGAT AG[gap/G]TAGGG CTTTACGCCTAG CTTCGAAA	gap	G			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3062	cg21411454	568	AGGGGGGTTGT GTACAGATAGTA GG[G/gap]CTTTA CGCCTAGCTTCG AAATGGAT	G	gap			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3063	cg21411454	574	TTGTGTACAGAT AGTAGGGCTTTA C[gap/C]GCCTAG CTTCGAAATGGA TAACGTC	gap	C			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3064	cg43040271	2038	CGTTTAAGAAGA TCATTAAGTGTA A[G/C]TTCTGCCG CCAGTGATGACG GAGGA	G	C			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.|pcls:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	
3065	cg40359282	1381	TTTTAAGTGCAC AAGTTGACTTGC C[G/A]TTTGCAGT GGGGTCGCCTA AGCGAC	G	A			SILENT-NONCODING	tm7	Human Gene Similar to SPTREMBL-ID:Q93127 G PROTEIN-COUPLED RECEPTOR - BALANUS AMPHITRITE, 379 aa.	2.10E-67	

3066	cg43040273	2989	TTTCTACTTTTAA AGACCCCCCCCC C[G/C]CCCAACA GAACACTAAACA GACTAT	G	C			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
3067	cg43040273	3473	GCTTCAGTTGTT TTCCCGAGCAAA G[gap/G]TCTAAA GTTTACAGTAAA TAAATTG	gap	G			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
3068	cg41554459	1566	ATGATGAATGAG ATGTAAATGTGC C[A/C]AGAATATA TTATATAAAGAAT TTTA	A	C			SILENT-NONCODING	tm7	Human Gene Similar to SWISSPROT-ID:P53453 D(2)-LIKE DOPAMINE RECEPTOR - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 463 aa.	9.10E-50	2
3069	cg43028527	2928	AAAATACAGCTG GATTGGGTTATG A[G/A]TATTTACG TTTTTGTAAATTA ATCT	G	A			SILENT-NONCODING	tnf	Human Gene SPTREMBL-ID:P78536 TNF-ALPHA CONVERTING ENZYME - HOMO SAPIENS (HUMAN), 824 aa.	0.00E+00	2
3070	cg43028527	3214	AAATATATATCTA AATTTAGAAATC[A/G]TTTGGGTTA ATATGGCTCTTC ATAA	A	G			SILENT-NONCODING	tnf	Human Gene SPTREMBL-ID:P78536 TNF-ALPHA CONVERTING ENZYME - HOMO SAPIENS (HUMAN), 824 aa.	0.00E+00	2
3071	cg43336100	1661	GGTATGTACCTT ATTACAAAAAAA A[T/gap]GATGAA AACATATTTATAC TACAAG	T	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
3072	cg43336100	35	AATTCGCGCTCA AACTCAGCTCAC T[T/gap]GAGAGT CTCCTCCCGCCA GCTGTGG	T	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)

3073	cg43336100	45	CAAACTCAGCTCACTTGAGAGTCTC[C/gap]TCCCGCCAGCTGTGGAAAGAACTTT	C	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
3074	cg44131329	1022	CCTGTGTTCTCTCCAAAGAGCAGAA[A/gap]GTGGGTACTATACGTGGCTACGTTG	A	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	2.90E-166	17
3075	cg44131329	2372	GACCCAGGCAGCAGCAGCATGGGGT[T/gap]GGCCAATGGGGCGGGTTCCACAGGA	T	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	2.90E-166	17
3076	cg43303573	272	TACATATATACATATACCACAAATA[G/C]AAAAATGACTGAAAGAAAAAAATAT	G	C			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	
3077	cg43303573	515	GTTTTGATCATCCTTTTTTTTTTTT[T/gap]TATAAGTGGCTAAATCTTCCAGCTA	T	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	
3078	cg43303573	516	TTTTGATCATCCTTTTTTTTTTTT[T/gap]ATAAGTGGCTAAATCTTCCAGCTAA	T	gap			SILENT-NONCODING	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	

3079	cg43965652	1131	TTTTTAAAAAAAAGAAATTCTGTTC[A/G]AAAGTATTTCAGACCAAAAGGAGGT	A	G			SILENT-NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3080	cg43965652	56	ATTAAAACTTGAAAGCTATGGCTTG[C/gap]CGCCATCAATGACGCCTATTGGGTT	C	gap			SILENT-NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3081	cg43965652	57	TTAAAACTTGAAAGCTATGGCTTGC[C/gap]GCCATCAATGACGCCTATTGGGTTC	C	gap			SILENT-NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3082	cg43965652	677	GTCTCTGAAAACTAAAATCAGACTT[T/C]AGATTCCTCTGAAACAGTTCTGGTT	T	C			SILENT-NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3083	cg43962131	136	AGAGGCGGCGTGGGACCAGACCCTC[gap/T]CCACAGCCAGCCTGGCCAAGGTGGC	gap	T			SILENT-NONCODING	tnfreceptor	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3084	cg43962131	210	AAGCACCCAGGGGTCTAGGAATGCT[C/gap]CCCCTTCTCTCCAGGGGCCAGAGGG	C	gap			SILENT-NONCODING	tnfreceptor	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3085	cg43962131	213	CACCCAGGGGTCTAGGAATGCTCCC[C/gap]CTTCTCTCCAGGGGCCAGAGGGGAG	C	gap			SILENT-NONCODING	tnfreceptor	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9

3086	cg43962131	214	ACCCAGGGGTCTAGGAATGCTCCCC[C/gap]TTCTCTCCAGGGGCCAGAGGGGAGA	C	gap			SILENT-NONCODING	tnfreceptor	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3087	cg43962131	89	CACTTTACCCGCAGCTGTGCTGTGC[A/gap]CCTCCCACACAGTGGTCTGAGCAGA	A	gap			SILENT-NONCODING	tnfreceptor	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3088	cg43985041	1779	GGCCAAGAGCAGAGGCAGCGAGTTG[G/T]GGAAAGCCTCTGCTGCCATGGTGTG	G	T			SILENT-NONCODING	tnfreceptor	Human Gene SWISSNEW-ID:P20333 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) - HOMO SAPIENS (HUMAN), 461 aa.|pdb:SWISSPROT-ID:P20333 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) - HOMO SAPIENS (HUMAN), 461 aa.	1.30E-255	1 (1p36.3)
3089	cg43984024	113	TAGGTCCCATTCTTTTTATTTGCAT[G/A]TGGTTACAATATAAATACACTTGCC	G	A			SILENT-NONCODING	tnfreceptor	Human Gene SWISSPROT-ID:P36941 LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR) - HOMO SAPIENS (HUMAN), 435 aa.	2.40E-242	12
3090	cg43335558	1176	AGACTCTGAGACAGTGCTTCGACAA[G/C]TTTGCAAACATGGTGCCCTTTGACT	G	C			SILENT-NONCODING	tnfreceptor	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8

3091	cg43335558	1183	GAGACAGTGCTT CGACAAGTTTGC A[A/G]ACATGGTG CCCTTTGACTCC TGGGA	A	G			SILENT-NONCODING	tnfrecept or	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
3092	cg43335558	1186	ACAGTGCTTCGA CAAGTTTGCAAA C[A/T]TGGTGCCC TTTGACTCCTGG GAGCA	A	T			SILENT-NONCODING	tnfrecept or	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
3093	cg43335562	1386	TCTGCCATGTCC TAAGTGTGATTC T[C/T]TTCAGGAA GTGAGACCTTCC CTGGT	C	T			SILENT-NONCODING	tnfrecept or	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
3094	cg43335562	1397	CTAAGTGTGATT CTCTTCAGGAAG T[G/C]AGACCTTC CCTGGTTTACCT TTTTT	G	C			SILENT-NONCODING	tnfrecept or	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
3095	cg43943896	372	AACAGCATGGAA GAGAACCAGTTT C[G/C]TTGCAGCT ACCTGGGAAGAC GGTTG	G	C			SILENT-NONCODING	traffic	Human Gene SPTREMBL-ID:P97412 LYSOSOMAL TRAFFICKING REGULATOR - MUS MUSCULUS (MOUSE), 3788 aa.	0.00E+00	1 (1q42.1)
3096	cg43988937	73	TTTTTTTTGAGTT ATTAAAAAAAAA[A/gap]CAAAAAAC ACAACCAAAAGA ACTGA	A	gap			SILENT-NONCODING	traffic	Human Gene SPTREMBL-ID:Q99408 PUTATIVE NUCLEOLAR TRAFFICKING PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 1410 aa.	0.00E+00	5 (5q32)
3097	cg43994751	532	CAGATTTAGGTC CATAAAAGAAAG G[gap/A]AAAAAA ATTATTCTAGTTA TATAAA	gap	A			SILENT-NONCODING	traffic	Human Gene Similar to SPTREMBL-ID:O08547 VESICLE TRAFFICKING PROTEIN SEC22B - MUS MUSCULUS (MOUSE), 215 aa.	1.70E-88	

3098	cg43934751	1050	GGCTGCCTGATC CAGGTGCACAG GC[C/gap]TCCGG TCACGGTTAAAG CCAAGCTG	C	gap			SILENT-NONCODING	traffic	Human Gene Similar to SWISSPROT-ID:Q02792 RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (EC 3.1.11.-) (P116) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1006 aa.	6.50E-55	
3099	cg43934751	709	CTCCCTCCACGA TCATCTCGTCTG G[G/gap]TGGATA CCCACCAGGCC CAGCTAGC	G	gap			SILENT-NONCODING	traffic	Human Gene Similar to SWISSPROT-ID:Q02792 RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (EC 3.1.11.-) (P116) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1006 aa.	6.50E-55	
3100	cg43995002	124	TTCAATGGAACA TCCCCGCTTTAG C[G/gap]CAGTGT TGAATCTAACAC CGAAAAA	G	gap			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3101	cg43995002	575	AAAACCCCACGC TTTAAACAAACAT [A/C]TTTGGGGGT GGCTATGGCACC TTGA	A	C			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3102	cg43995002	77	TTTTTTTTTTTT TTTTTTTTTTT[T/A]GAAAACCACA CTGCTCTTTTATT CA	T	A			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3103	cg43995002	79	TTTTTTTTTTTT TTTTTTTTTG[A/T]AACCACACT GCTCTTTTATTCA AT	A	T			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3104	cg43995002	80	TTTTTTTTTTTT TTTTTTTTTGA[A/T]AACCACACTG CTCTTTTATTCAA TG	A	T			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11

3105	cg43995002	791	AGATAAAGAAGT AACAAAGGAAAA A[G/A]AAAAAAAT TAATAAAAATTTC ACGA	G	A			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3106	cg43948839	329	GGTGCCTGCAG AGCAAGGAGGG GGG[C/gap]CCCC CAAAATGGCTCG GCCCCTGCA	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.|pcls:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0.00E+00	17
3107	cg43949599	376	CACCCCACCTTG GATTGGGCCGC AG[G/gap]TGTGG AGGGCCTCATCA AACTCTTT	G	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P17480 NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90) - HOMO SAPIENS (HUMAN), 764 aa.	0.00E+00	17
3108	cg44027791	185	ATACCTCAAGCA GTTACAACTAAA A[A/T]TAAAGTTG GATTTTTGTTTAA TTTA	A	T			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
3109	cg44027791	572	ACAGTGTTCATC ATCTGAAGTAGA G[A/gap]GTATAA GGCAACGTTCTC CATAGAA	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
3110	cg44027791	60	GTTATTTTGAAG ATTTTGCCTCAG G[gap/C]AACTAA ATTTATTAGCAA GAAAAAA	gap	C			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

3111	cg43328754	22	GGAATTCCTTTT TTTTTTTTT[T/G]T GGCTCAAAAACT CATCTTTATTGG	T	G		SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I-REL) - HOMO SAPIENS (HUMAN), 579 aa.	0.00E+00	19
3112	cg43933098	417	CAGCCTGAGGAT GAGGCACAGGG AG[G/gap]CAGGG CCCATCACTCAG GAGGCCAT	G	gap		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3113	cg43933098	425	GGATGAGGCAC AGGGAGGCAGG GCC[C/gap]ATCA CTCAGGAGGCC ATGGGAGAAA	C	gap		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22

3114	cg43933098	458	AGGAGGCCATG GGAGAAACAGTC TC[C/T]GGGAGG TGCTGCACCTGG GGACCCA	C	T			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pcls:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3115	cg43933098	57	TTTTTTTTTTTTT TTTTTTTTTTT[T/G]TTGGGTGGTA CCAATCTGTGTT TAT	T	G			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pcls:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3116	cg43933098	58	TTTTTTTTTTTTT TTTTTTTTTTT[T/C]TGGGTGGTAC CAATCTGTGTTT ATT	T	C			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pcls:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22

3117	cg43933098	582	CCCTCTGCCCAC TCTGAAAAGAGG G[G/gap]CTTGCC GCTGGGGAGGG ATTAGGGG	G	gap		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pdb:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22	
3118	cg43933098	704	CCTCAACTTACC ATGGGGTTACTT C[C/T]TGATAAAC CCATCATAAATG AAAAT	C	T		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.|pdb:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22	
3119	cg43934374	5006	AGTGAACATATG CCACTGCCTGGC C[T/C]TTTTTTCTT CAGAGCTTGTTG TCTT	T	C		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX-BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.|pdb:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX-BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	15 (15q21)	

3120	cg43921342	2083	GGTTTTGTTTAC TGGAAAAAAAA A[A/gap]ATGCTC CTGTCAGCCCAG GCAACAG	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.|pcls:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0.00E+00	
3121	cg43921342	2084	GTTTTGTTTACT GGAAAAAAAAA A[A/gap]TGCTCC TGTCAGCCCAGG CAACAGG	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0.00E+00	
3122	cg43936136	1135	ATGCCAGTGTGA CTCTTAAAACCT T[C/T]CCATCTGG AGTCCTGTATTT TCTCT	C	T			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q99840 TRANSCRIPTION FACTOR NFATX2 - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	
3123	cg44028034	254	CAGAACACAGCC AGTTACGCAACA G[C/gap]GCAAGG CCTGCTCCAGGC CCCACCT	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P42230 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 5A (MAMMARY GLAND FACTOR) - MUS MUSCULUS (MOUSE), 793 aa.	0.00E+00	

3124	cg44130900	1668	TTAGTACACAGA AATTCTGCAGAT G[C/G]TATTGTAC ACATGTGACAAC CTATG	C	G			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
3125	cg44130900	2140	TTGTATCCAGAA ATGTATACTCAT C[G/A]TATTTTAA AGCTAAATTTATT TTTT	G	A			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
3126	cg43968711	277	TTAGGAGAAACA TCTTTTATTTCTT[C/G]TAAAGAGGT GAAAATAAGATT TTTT	C	G			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3127	cg43968711	286	ACATCTTTTATTT CTTCTAAAGAGG[T/G]GAAAATAAG ATTTTTTTAATAT TTC	T	G			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3128	cg43968711	303	TAAAGAGGTGAA AATAAGATTTTTT [T/gap]AATATTTC TCACTCATAAGA TTTTT	T	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3129	cg43968711	351	TTTAAACTCTTAA AAATGCAATATC[T/C]TCTTTTCAAA GCACATGCCATC TTA	T	C			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3130	cg43968711	467	AATTCTGCATTA AAAAACCCTATG C[G/A]ACTTTCTG CAAATATATTCC CTCTT	G	A			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11

3131	cg43968711	473	GCATTAAAAAAC CCTATGCGACTT T[C/T]TGCAAATA TATTCCCTCTTTA TTAT	C	T			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.3E-292	11
3132	cg43968711	486	CTATGCGACTTT CTGCAAATATAT T[C/G]CCTCTTTA TTATTCAGGGAC TCCAA	C	G			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3133	cg43968711	557	TATTTATCGTTTC TTATTTCCGTAG[G/gap]AAACACAG AACCAATGATGT CTTCT	G	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3134	cg43968711	566	TTTCTTATTTCCG TAGGAAACACAG [A/G]ACCAATGAT GTCTTCTGACAA CTGT	A	G			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3135	cg43947662	2433	GGCCCCCTCCCT CCCAGGTCTCGC T[G/gap]CTCTCTT TCCCCTCCAGGC CTCGCT	G	gap			SILENT-NONCODING	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.70E-276	12
3136	cg43947662	2462	TCTTTCCCCTCC AGGCCTCGCTTC C[T/gap]GGTCAG TCCCACGATCAC TTCCGGT	T	gap			SILENT-NONCODING	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.70E-276	12
3137	cg43011561	1783	AGGCTTGGTCCA ATACATGGCTCT G[C/gap]CCCCCA GAACTTAAGGCT CTCACTG	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TFIIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.30E-275	19 (19p13.3)

3138	cg44024015	1729	CCGGGATGGGC CGACCAAACCCT TA[G/C]CAGCCC AGCATTTCCCGA AGCCCGA	G	C			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3139	cg44024015	2456	TGTGTCCCCTTT ACTGAGCGCACA G[C/gap]CACAGC CTGTCTTGTCAG GTGGACC	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3140	cg44024015	2457	GTGTCCCCTTTA CTGAGCGCACA GC[C/gap]ACAGC CTGTCTTGTCAG GTGGACCC	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3141	cg43917801	175	ATACATTTATTCA TGCCAGTCTGTT[G/A]CATGCAGGC TTTTTGGCTTCC TACC	G	A			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3142	cg43917801	2344	AGAAAGAAAAAG TAAGCAGGGCTG G[C/gap]TTCGCC CGCGTTCTCGTC GTCGGAT	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3143	cg43917801	3091	GGGAGCTGGCG GCGGCGGCTGC TGG[G/gap]CCTC CGCCTTCTTTTC TACGTGAAA	G	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)

3144	cg43917801	377	GGAATCAACTGC TTCAGGGAAAAA G[A/gap]AAAAAA AAAAAAAAAAGA CTTGCCT	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3145	cg43917801	393	GGGAAAAAGAAA AAAAAAAAAAAA A[A/gap]GACTTG CCTGGGAGGCC GCGAGAAA	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3146	cg43917801	635	GGACTTTTCTCT CTTTACCCACCT C[C/gap]GCCCCT GCGAGGAGTTG AGGGGCCA	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3147	cg43917801	654	CACCTCCGCCCC TGCGAGGAGTTG A[G/gap]GGGCCA GTTCGGCCGCC GCGCGCGT	G	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3148	cg43917801	657	CTCCGCCCCTGC GAGGAGTTGAG GG[G/gap]CCAGT TCGGCCGCCGC GCGCGTCTT	G	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.|pcls:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3149	cg42906458	22	TTTTTTTTTTTT TTTTTTTT[T/G]TT AGCTATCATAAC TTTATTAAACA	T	G			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q92759 TRANSCRIPTION FACTOR TFIIH - HOMO SAPIENS (HUMAN), 462 aa.	4.20E-245	

3150	cg43920700	1897	GCCTTCCTCCCCCTGACCCCGCCCC[G/C]GCCTTCTGGGGAAGGAACAAAGTCC	G	C			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1/X (NFI-X) (NF-I/X) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.10E-243	19 (19p13.3)
3151	cg43918762	1031	AAGATCAGATAAATAAAAAAAAAAA[A/gap]GGCTTAAAACAGACTCACCATATTT	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3152	cg43918762	1452	TTTGTTGTTTTGTTTAAAAAAAAAA[gap/A]GGGTTCACAAACTTGGCAGAACTTT	gap	A			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3153	cg43918762	699	GTGGAATAAAATAAACTTTTTTTTT[T/gap]CTCCCTACAATACATAGAAGGGTTA	T	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3154	cg43998635	277	TGCTGAGAAAGAGGAAGGAGTCTCC[T/A]TGAGCTCCAGCATCAGGGGCAGAAA	T	A			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P43694 TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4) - HOMO SAPIENS (HUMAN), 442 aa.	1.60E-236	8 (8p23.1)
3155	cg43129605	1480	CTTGGAGGGACCAGGGTTTCCAGAG[A/T]AGCTCACCTTGTCTCTGCAGCCCTG	A	T			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20

3156	cg43129605	1481	TTGGAGGGACCAGGGTTTCCAGAGA[A/T]GCTCACCTTGTCTCTGCAGCCCTGG	A	T			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3157	cg43129605	1811	TCCACATGTGTGTGCATGAGTCCAT[G/C]TGTGCGCGTGGGGGGGCTCTAACTG	G	C			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3158	cg43129605	1813	CACATGTGTGTGCATGAGTCCATGT[G/C]TGCGCGTGGGGGGGCTCTAACTGCA	G	C			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3159	cg43129605	1857	AACTGCACTTTCGGCCCTTTTGCTC[T/G]GGGGGTCCCACAAGGCCCAGGGCAG	T	G			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20

3160	cg43129605	1858	ACTGCACTTTCG GCCCTTTTGCTC T[G/T]GGGGTCC CACAAGGCCCA GGGCAGT	G	T			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
3161	cg43129605	2054	TTGGTGAGCCTG GGGAATCAGCAA A[gap/A]GGGGAG GAGGGGTGTGG GGTTGATA	gap	A			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3162	cg43129605	2265	TCTCCAGGGGG CCAGTTCAGGGC CC[C/gap]AGCTG CCCCCCAGGAT GGATATGAG	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3163	cg43921348	341	GCCCACCCAGA CCTAGGGGCAG GGC[C/gap]AGGA GCAAAACAAGAG GGAGAGGCA	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.|pcls:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.	3.80E-228	

3164	cg43984259	363	CCTGCAGGTTCTAGGGCTAAAGGCC[C/gap]AGCAGAAGTGGGCACGTGAGAGGGC	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
3165	cg43984259	457	GCTAGAAGTGGTGCTGGCATGTGCC[C/gap]AGTTCCACCCCACCCTTCCCTCCTA	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
3166	cg42345420	223	CTTCACCTATAATGCAACTAATCAT[G/C]TACTTAGTTGCTATGTTAATCTATT	G	C			SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR - HOMO SAPIENS (HUMAN), 399 aa.	1.50E-210	
3167	cg42479822	235	GTAATATTTTACCAAAAAAAAAAAA[gap/A]GAAAAAGTGAACAGTCTGCCAGTGT	gap	A			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06547 GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA 2) - HOMO SAPIENS (HUMAN), 383 aa.	2.00E-197	15
3168	cg42479822	433	AAAGCAATTTTTTTCCGTAAGAATC[A/G]TTTCCTGGGGAGAAATAAGTCCATA	A	G			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06547 GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA 2) - HOMO SAPIENS (HUMAN), 383 aa.	2.00E-197	15
3169	cg21646034	93	TGTGTGTAGCGGGGCCGCGTCAGCC[C/gap]GGCCGGGTACGAGGCGCCTCGGGTC	C	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15

3170	cg21646034	97	TGTAGCGGGGC CGCGTCAGCCC GGC[C/gap]GGGT ACGAGGCGCCT CGGGTCCCCG	C	gap		SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15
3171	cg43998970	1481	CCACAGACTGAG CTGGCCCAGAG GG[G/gap]TGGAA CTGCTGATGGGA TTTCCTTC	G	gap		SILENT-NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
3172	cg43947199	1485	AATATGTTTTGAA ACAGGTACCATA[C/A]AATTATTATA TGGTCTCCCTAC TGA	C	A		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.|pcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3173	cg43947199	236	AAACATTATTTCA AAAATGTACTTT[G/C]TTTTTGAAAT AAAACAAAATCT TCA	G	C		SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.|pcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8

3174	cg43947199	299	CAAATAGAGGT GAGTTGGTACCA G[T/C]GGGCCAA TTCTTAACACGG ACATTT	T	C			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. lpcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3175	cg43947199	423	CAAAGCATGTAC TGAGGTCTTTCT A[C/T]GGGTGCC TGACAGAATGCA GATTCA	C	T			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. lpcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3176	cg43947199	550	ACAATTTTTGTCT TACTCCAAACAG[A/gap]AAAAAATG GTACACACTTTA ACAAA	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. lpcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8

3177	cg43947199	556	TTTGTCTTACTC CAAACAGAAAAA A[A/gap]TGGTAC ACACTTTAACAA AAGCAAA	A	gap			SILENT-NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.|pcls:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3178	cg43948504	483	GAGTTTGGTAAT TTGCACTTGTTTT [gap/T]GTAAACT GAACTGCTCCTC TCCTCA	gap	T			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P29084 TRANSCRIPTION INITIATION FACTOR IIE, BETA SUBUNIT (TFIIE-BETA) - HOMO SAPIENS (HUMAN), 291 aa.	9.50E-152	8 (8p21)
3179	cg43948504	515	GAACTGCTCCTC TCCTCAGCCGCA A[gap/A]GAAGCA GATAGGAAGACA GTCTTCA	gap	A			SILENT-NONCODING	transcript factor	Human Gene SWISSPROT-ID:P29084 TRANSCRIPTION INITIATION FACTOR IIE, BETA SUBUNIT (TFIIE-BETA) - HOMO SAPIENS (HUMAN), 291 aa.	9.50E-152	8 (8p21)
3180	cg43992817	137	TGGAAGAATCAG TTCGAAGACATA A[T/A]AGCCTTTA CTTTTTTCTTTTA TTAT	T	A			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
3181	cg43992817	499	GGGTTGGGGAG TTTAGGAGGAGG GG[T/C]GGCCTG AGCCCCCTCAGT TCCGCCA	T	C			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3

3182	cg43992817	508	AGTTTAGGAGGA GGGGTGGCCTG AG[C/gap]CCCCT CAGTTCCGCCAC GGCCTCCA	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
3183	cg43935832	3340	AAACTGGTGCAT ACTGGCATTGGC C[C/gap]TTGGTG GGGAGCACAGA CACAGGAT	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:P42224 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) - HOMO SAPIENS (HUMAN), 750 aa.|pcls:SWISSPROT-ID:P42224 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) - HOMO SAPIENS (HUMAN), 750 aa.|pcls:TREMBLNEW-ID:G2281071 TRANSCRIPTION FACTOR ISGF-3 - HOMO SAPIENS (HUMAN), 750 aa.	3.20E-144	
3184	cg43299377	1472	TGGTACAAAGAA TAGATGCAGGCA G[C/T]CATAGGTA CAAGGGATTCCC TTAAT	C	T			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3185	cg43299377	1635	TGAGATGACGTT AACAGGACCCCT G[G/gap]CCAGTT TCCATGAGATCT GGGTCTC	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)

3186	cg43299377	1666	TTCCATGAGATC TGGGTCTCTGTC A[C/T]TTTCAGGG GGTAGGCTCCTG GAGGC	C	T			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3187	cg43299377	1840	GAGAGACCTGG GGATGTAGGTGC CG[G/gap]CTCCG CAGGGCTAGTAA GCAGTTCT	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3188	cg43299377	524	CAAAGTGCTGGG ATTACAGGCGTG A[G/gap]CCACCG CGCCTGGCCCG GCAGCCCT	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3189	cg43283688	1091	GAGTTTTATAAAT TAAAAGGTCAAA[A/C]CTGAAGCTT TTTATTTAGGCTT TTC	A	C			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:P18846 CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1 (TREB36 PROTEIN) - HOMO SAPIENS (HUMAN), 271 aa.	1.90E-137	12
3190	cg43283688	1092	AGTTTTATAAATT AAAAGGTCAAAA[C/A]TGAAGCTTT TTATTTAGGCTTT TCC	C	A			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:P18846 CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1 (TREB36 PROTEIN) - HOMO SAPIENS (HUMAN), 271 aa.	1.90E-137	12
3191	cg44012692	2080	CTCTTGCACCTG AGAGTGGGAGTT T[C/T]GTAGGAAC ACAGGAAGGAG ACCAAC	C	T			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9

3192	cg44012692	4499	ATCACCCCGACG CGGGTGGCGAG GG[T/C]CCCGCC GAGCGCCAGGT CTAAGAGA	T	C			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9
3193	cg44012692	4581	AACCCCTGCTCC GGCCGGTCCGC AC[C/gap]GTTCC GGCATTCTCTTG CTCAGTAA	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9
3194	cg43982109	1896	AGTGACCCGACC CCAATCTCGGAG A[G/gap]CCTCCT GGCAATACACAA CTCCAGC	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.60E-131	10 (7p)
3195	cg43310921	98	TGTTCCTTCAAA TTAAAAAAAAAA [gap/A]TACAAAA GCTACGTAGAAA ACGTCA	gap	A			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:O00112 LIVER-SPECIFIC BHLH-ZIP TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 429 aa (fragment).	7.20E-124	19
3196	cg43263063	174	GCGCAGGCCCC GCAGCCGGGCC AGC[G/C]CGCCG CCCCCGGCCGC GGCTGCCTC	G	C			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13887 TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2) - HOMO SAPIENS (HUMAN), 219 aa.	3.50E-122	
3197	cg43263063	491	CACCAGAGTGAA ACGACTGCCCCT C[C/gap]TCCGGC CCCGACCCAGG CCCTCCCT	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13887 TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2) - HOMO SAPIENS (HUMAN), 219 aa.	3.50E-122	

3198	cg43918209	934	CGATGGCTCCCC GGGGACAGAGT CC[C/gap]TCTCC GGGCCTCTCAG CAGCCCGGG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3199	cg43918209	105	TCTAACAAAACG CCAGGTAGACG GA[G/gap]TTAAA AAGAATCCACCG CACGAAAG	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3200	cg43918209	1841	CAGGTGCACTCC GGACAACGGGC TC[G/T]CTCACGC CTCTCTACACAA ACCAAC	G	T			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3201	cg43918209	346	CGCTGGAACCTG GGAACCTACTGG G[C/G]ACCTCTAA TGCAGATGAGAA AAACT	C	G			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3202	cg43918209	490	GCCACTCTCCTC CCCACTGCCCAG G[G/gap]CGGGTG CACGCCCCAGG ACCTCCTC	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3203	cg43918209	511	AGGGCGGGTGC ACGCCCCAGGA CCT[gap/T]CCTC CCAGGCCCCAC ACCCACGCAA	gap	T			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3204	cg43918209	517	GGGTGCACGCC CCAGGACCTCCT CC[C/gap]AGGCC CCACACCCACGC AAGGCGAC	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19

3205	cg43918209	524	CGCCCCAGGAC CTCCTCCCAGGC CC[C/gap]ACACC CACGCAAGGCG ACAGGAAGC	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3206	cg43918209	532	GACCTCCTCCCA GGCCCCACACC CA[C/G]GCAAGG CGACAGGAAGCT CCCCACG	C	G			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3207	cg43918209	533	ACCTCCTCCCAG GCCCCACACCCA C[G/C]CAAGGCG ACAGGAAGCTCC CCACGC	G	C			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3208	cg43918209	869	GTCTCTGCGGAA GGCGCCCGCGC CC[C/gap]CGGCT CAGACTCCTCGG TGCCGTCC	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3209	cg43918209	870	TCTCTGCGGAAG GCGCCCGCGCC CC[C/gap]GGCTC AGACTCCTCGGT GCCGTCCC	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3210	cg43918942	203	CATGGGGAGGA TGAGGCCCCTG GGG[G/gap]TCAG TGAGGCACGGC TCTGCCTCAA	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

3211	cg43918942	290	TCGGCCACATCCGGGGCAGCCATGC[C/gap]AGAGCTGAGACCTCCTACGAGTGGT	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3212	cg43918942	476	GCCAGGACACTATGCAGGCTATGCC[C/gap]GCACTGCCTACAGAGCTATGCTCAG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3213	cg43918942	544	CTCAGCTGTCGGGCACTCAGTTCAC[C/gap]TGCCGGCAGCCGCAGGCGCTCCTGG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3214	cg43918942	93	AAGCCCTCGAGAAGCCCTGGCAGGA[A/C]CCAGGCTGGCTACTGAGCTCTGGGC	A	C			SILENT-NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3215	cg43993354	1336	CCACCCCGCCCCCAGTGCTGGGGCG[G/gap]CCCCGGCTCCGGCCCCTGGGGGAGC	G	gap			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.|pcls:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)

3216	cg43993354	1377	CTGGGGGAGCG CCAGCGGGTGG TGA[T/C]CAGAGC AGGGCCCACAC CCCGGCAG	T	C			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.|pcls:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)
3217	cg43993354	1508	GGTGATTGGATC TGGCCAGAAAG GC[gap/C]AGCCA TGCCGAGGTCC CAGGGGACG	gap	C			SILENT-NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.|pcls:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)
3218	cg43995484	3358	TGGAAGAAAGAA GCATTGAAAACA A[A/C]GACATTCT TCCCACTTCTTG GATTT	A	C			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSPROT-ID:Q62318 TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1) - MUS MUSCULUS (MOUSE), 834 aa.	1.80E-96	-
3219	cg42930883	1095	GGAAGGAGACA CATTCACAAAGA AA[C/A]GTTGCGA AAATTGCGAAAT CTGTTG	C	A			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)
3220	cg42930883	1125	CGAAAATTGCGA AATCTGTTGTGC A[T/C]GCTCAAAT GAAAACGCCTTT CGGCT	T	C			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)

3221	cg42930883	1348	TTAATGTATTTTT GTAAATAGTTTA[A/G]CACTTTCTTT TTTTACGTAAAC CTG	A	G			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)
3222	cg43051067	1933	TGTCTGTACTTT ACAATTCAACTA C[A/T]TGTTCTAC CCAGCATTTAAC GGCAA	A	T			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.|pcls:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.30E-91	
3223	cg43297584	222	ACTTGCGACAAG TTGCCGGAGCC GC[G/gap]GGGC GCGGGCGGCGG ACAGATTGAC	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.60E-90	
3224	cg43917302	1743	CATTCACGGCGA AGCCGCCACGC GG[C/gap]CCCGG ACGCCGCCCTTG CGGCCCAG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.|pcls:SWISSPROT-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7
3225	cg43917302	1802	GCTCCCCCCGA GGTGGCGCCGC CCC[C/gap]GCTC TTCTTCTGAGCC TAGTTCTCA	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.|pcls:SWISSPROT-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7

3226	cg43917302	1949	GCCGCGGGACA CCTGTTTCCTTC CC[G/gap]CAGTG TCTGCGTCCGCA CAGCATAC	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.|pcls:SWISSPROT-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7
3227	cg43917396	497	GACTTGCCAGAC GAGGCTCTATTC C[G/gap]GGCTGC TGCAGCCCACTT TTCTCCT	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3228	cg43917396	660	TCCCGGCCTGG GGAGAGGGCTC GCT[G/gap]GCTC TCCAGCCCACTC ACCAGTCTC	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3229	cg43917396	677	GCTCGCTGGCTC TCCAGCCCACTC A[gap/C]CCAGTC TCTGGATGCTCT GCAGTTC	gap	C			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3230	cg43917396	679	CTCGCTGGCTCT CCAGCCCACTCA C[C/gap]AGTCTC TGGATGCTCTGC AGTTCAT	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3231	cg43917396	76	CCCCTGGGGAC TCAAGGCAGAAG TG[C/gap]CACTC CCTCCGTTGACC ACGGCTGG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	

3232	cg42702130	675	GAGGGGCACAC AGACTGTGGCAG AG[C/gap]TGCGC CCATCCCGCAGA GGCCCCTG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3233	cg42702130	706	CCATCCCGCAGA GGCCCCTGTCCA C[C/A]TGGAGAC CCGGAGACAGA GGCCTGG	C	A			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3234	cg42702130	899	AGTCCCATGGCA CAGAGCAAGGC GG[G/gap]CAGGG AACGGTTATTTTT CTAAATA	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3235	cg43317047	1468	GAAGCTACTGTT TTCTCTTTTGTTC [A/G]TTTTACCTC TTTCTTACTCTTA CTA	A	G			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSPROT-ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	3.80E-61	6
3236	cg43944978	227	TTGTGGTAAATT TTTTTATCCTAAA [A/gap]CAACTCA CCTTGGCCGAAA AATGGG	A	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3237	cg43944978	284	CCCAAGGTCCCC TACTAGGCCGGA G[G/gap]AGAAAA GGACCTACCTCC TACAGGG	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3238	cg43944978	339	AAACAAGGGAGA CTAGGACTCAAT G[G/gap]TCGCCC AAGGCCCAAGG GTCTCCAG	G	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17

3239	cg43944978	591	ACTGAGCCTCTGGATCAGCACCCTC[T/C]GATAGGAAGCAAGGAAGCACACTAC	T	C			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3240	cg43922509	38	TGCTTTTTTTTTTTTTTTTTTTT[T/G]TGTCTTTCATAGAGTTTATTTGAAA	T	G			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSPROT-ID:P14741 TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCN3) (GCD COMPLEX SUBUNIT GCN3) (TRANSCRIPTIONAL ACTIVATOR GCN3) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 305 aa.	1.20E-55	12
3241	cg42746806	143	GGAATTCGCCCACGCAGGAGGCAGG[G/C]CGCTGCGGAGACCCCAGGGCTACGA	G	C			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:O00343 BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 113 aa (fragment).|pcls:TREMBLNEW-ID:G1732371 NEUROGENIC BHLH TRANSCRIPTION FACTOR - RATTUS NORVEGICUS (RAT), 113 aa (fragment).	2.00E-55	
3242	cg42746806	145	AATTCGCCCACGCAGGAGGCAGGGC[G/T]CTGCGGAGACCCCAGGGCTACGAGA	G	T			SILENT-NONCODING	transcript factor	Human Gene Similar to SPTREMBL-ID:O00343 BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 113 aa (fragment).|pcls:TREMBLNEW-ID:G1732371 NEUROGENIC BHLH TRANSCRIPTION FACTOR - RATTUS NORVEGICUS (RAT), 113 aa (fragment).	2.00E-55	
3243	cg44928765	237	CTGCAGAGACTTAAGTTCTCTTTGC[C/T]CCAGTGCCCAGACCTGCCTTCTCTT	C	T			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSPROT-ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	2.10E-53	16

3244	cg44928765	421	GTAAGGGGGAG GAGAAACACAAA CA[C/T]CTTCCGT GTGAATCTAAAG CATGGA	C	T			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSPROT-ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	2.10E-53	16
3245	cg43979598	1031	CACCCTAAAAGG TTAGGTCAGGCT C[C/A]TCCCAGTG GCCTTCAAAAAA TAAAT	C	A			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3246	cg43979598	134	AAACAGTGGAGA CGAGTGTAGCAC T[G/A]TCCCCCAA ATCACCAACCCC CAGGT	G	A			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3247	cg43979598	178	CCCAGGTCCCAA GGCCTGGGCTG GG[C/gap]CAGCG CTAACAGGTGAG CCCAGGAG	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3248	cg43979598	179	CCAGGTCCCAAG GCCTGGGCTGG GC[C/gap]AGCGC TAACAGGTGAGC CCAGGAGT	C	gap			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3249	cg43979598	563	TGGAGTACTGGC TGGAGGGCCCC CC[gap/C]AGACG GGGACCACCCC CCAAAAAAA	gap	C			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3250	cg43979598	703	CCCTGGCCAAAA AGTTGGTTGAAA A[gap/A]GGATAA GCTGTCTGAGAG AAAGGTT	gap	A			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)

3251	cg43979598	732	AAGCTGTCTGAG AGAAAGGTTGGG G[gap/G]AGGTGG AAATTTCTATTCC AAGGGT	gap	G			SILENT-NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3252	cg41074975	149	GGAAAAGCCAG CGAGAGGCAGG TGT[G/C]TAAAGG GAGCCTCTCAGC ATGCAGG	G	C			SILENT-NONCODING	transcript factor	Human Gene Similar to SWISSPROT-ID:Q13263 TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1) - HOMO SAPIENS (HUMAN), 835 aa.	5.70E-51	11
3253	cg43946772	1795	ACTACTGATGTG CAAGCAAACCAT A[A/G]AAGGTACA GTTCTCCAGAAA GCATA	A	G			SILENT-NONCODING	transfera se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,O N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3254	cg43946772	895	TCTTTGGCTAAG TCATTTAAAAATT [T/C]TTTTTAAAC ATTTTCAGTCAA ATTT	T	C			SILENT-NONCODING	transfera se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,O N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3255	cg43946772	896	CTTTGGCTAAGT CATTTAAAAATTT [T/C]TTTTAAACA TTTTCAGTCAAAT TTT	T	C			SILENT-NONCODING	transfera se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,O N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3256	cg42166807	1619	AGAAGAATCCTT TGACTGAAGCAT G[A/T]ATGTAGAC TCGAAAGTACAG CATGG	A	T			SILENT-NONCODING	transfera se	Human Gene SWISSPROT-ID:Q09328 ALPHA-1,3(6)-MANNOSYLGLYCOPROTEIN BETA-1,6-N-ACETYL-GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE) (N-ACETYLGLUCOSAMINYL-TRANSFERASE V) (GNT-V) (GLCNAC-TV) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)

3257	cg42166807	1672	TAGTCTAGTATAAGGGATCGGATCA[G/T]TGCTCAGCCTCTCCCTTGAGTGACA	G	T			SILENT-NONCODING	transferase	Human Gene SWISSPROT-ID:Q09328 ALPHA-1,3(6)-MANNOSYLGLYCOPROTEIN BETA-1,6-N-ACETYL-GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE) (N-ACETYLGLUCOSAMINYL-TRANSFERASE V) (GNT-V) (GLCNAC-TV) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)
3258	cg43916882	141	CTCAGCTCACTGCAAGCTCTGCCTC[T/C]TGGATTCATGCCTTTCTCCTGCCTC	T	C			SILENT-NONCODING	transferase	Human Gene SWISSPROT-ID:P39656 DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
3259	cg43916882	533	TCCCACGGCTTTAAACAAAGCAAAA[C/A]AAAACCACCAATCCTAATAACCCCC	C	A			SILENT-NONCODING	transferase	Human Gene SWISSPROT-ID:P39656 DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1

3260	cg43916882	563	CCACCAATCCTAATAACCCCCCTCC[C/T]TGCCCCGTCTCCACGCTGTGCGGAG	C	T			SILENT-NONCODING	transferase	Human Gene SWISSPROT-ID:P39656 DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
3261	cg43948635	1630	TTTGGAGCAGCTCATCCATCTCTCA[G/A]GTGGGGGTCCTCCGGCAGGCAGCTT	G	A			SILENT-NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3262	cg43948635	816	CAATGCCAAACACATAGTATGAGAA[T/G]TTTACTTTTTAAGAAATTAATTTAT	T	G			SILENT-NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3263	cg43948635	818	ATGCCAAACACATAGTATGAGAATT[T/G]TACTTTTTAAGAAATTAATTTATTT	T	G			SILENT-NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3264	cg43948635	985	TGCACTTCAGCTACGTGAAAATAAA[A/G]TTTCTTTGGGAAGGTGACATTTGGC	A	G			SILENT-NONCODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3265	cg43311354	1596	GAGAACACAGTGGCTGGTTTTAAAA[A/gap]TTCTTTCCACACCTGTCAAACCAAA	A	gap			SILENT-NONCODING	transferase	Human Gene TREMBLNEW-ID:G385673 FARNESYL-PROTEIN TRANSFERASE BETA SUBUNIT, FTPASE BETA SUBUNIT=PRENYL-PROTEIN TRANSFERASE DPR1/RAM1 HOMOLOG - BOS TAURUS, 437 aa.	8.50E-238	14 (14q23)

3266	cg44017777	229	ACATCATTCCTTTG TGATCTCCTGTG[G/T]ATCCCTATA GTTATTTCAAGT AAAG	G	T			SILENT-NONCODING	transfera se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP-RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)(+)–ARGININE ADP-RIBOSYLTRANSFERASE) (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9.00E-195		
3267	cg43995237	239	GTATACACAAAG AACTGTAGTCAG A[A/T]TAACAGGA CTTCAGAATAAA AAGCA	A	T			SILENT-NONCODING	transfera se	Human Gene SWISSPROT-ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182		1
3268	cg43258046	495	ATGTGGTGAACT GGATGTGCTACC G[C/gap]AAGACA GAGGACTTCTTC ACCATCT	C	gap			SILENT-NONCODING	transfera se	Human Gene Homologous to TREMBLNEW-ID:G2673964 LECITHIN:CHOLESTEROL ACYL TRANSFERASE - AKODON TORQUES, 294 aa (fragment).	3.20E-146		16 (16q22.1)
3269	cg44000740	274	TGCTCTGGGACT TGGGCAAGTCTT A[A/G]GCAAGCC ATTCCTGCTTTC TGGGCC	A	G			SILENT-NONCODING	transfera se	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS-THETA) - HOMO SAPIENS (HUMAN), 239 aa.	1.60E-117		16
3270	cg43949162	109	TTACAGCTCAGA GGAGAGTCATTT A[C/T]TAGACATT CGGTTGTTATTA AACAC	C	T			SILENT-NONCODING	transfera se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115		6

3271	cg43949162	18	TTTTTTTTTTTTTTTT[T/A]TCAATGACTCATAAATTCTTTATTT	T	A			SILENT-NONCODING	transferase	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
3272	cg43949162	51	CTCATAAATTCTTTATTTTGGCTAA[C/T]ACTGATTGCATTCATTACTACCATT	C	T			SILENT-NONCODING	transferase	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
3273	cg43920566	1312	ATGTCTAGCAGCAGATTTTTTTTTT[gap/T]ATTGGTACATATTATCCTTCAAATC	gap	T			SILENT-NONCODING	transferase	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3274	cg43920566	1845	ACAGGATGTTGCTTACCAGGACGGA[G/gap]TTTTGGTATCTTAGTACTGAAGTTA	G	gap			SILENT-NONCODING	transferase	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3275	cg43920566	2268	GGTTTTTCCTGCCACAGGATATAAC[T/gap]TTTTTTTATATAACAAGCATAACAC	T	gap			SILENT-NONCODING	transferase	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3276	cg43920566	2275	CCTGCCACAGGATATAACTTTTTTT[T/gap]ATATAACAAGCATAACACACCACTG	T	gap			SILENT-NONCODING	transferase	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3277	cg43928442	40	TTTTTTTTTTTTTTTTTTTTTTTT[G/T]TTTTGCCTGATGGCATTAGGTTTAT	G	T			SILENT-NONCODING	transferase	Human Gene Similar to SPTREMBL-ID:O09034 GLUTAHIONE S-TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa.	2.60E-87	7

3278	cg43954704	359	GTTGCTCCTGTC CTGGGGGGCTC TG[C/gap]CTCCA CCTCCCAGTCCA GGATGTCT	C	gap			SILENT-NONCODING	transferase	Human Gene Similar to SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,O N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.10E-68	2
3279	cg43954704	360	TTGCTCCTGTCC TGGGGGGCTCT GC[C/gap]TCCAC CTCCCAGTCCAG GATGTCTG	C	gap			SILENT-NONCODING	transferase	Human Gene Similar to SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,O N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.10E-68	2
3280	cg43266642	220	GAGGGGGAGGG CCTCCGAGTTCC CA[A/G]ACAAAAC ACAGGTACCTAA GGGCTT	A	G			SILENT-NONCODING	transferase	Human Gene Similar to TREMBLNEW-ID:G2688966 CARNITINE ACETYL TRANSFERASE - MAGNAPORTHE GRISEA (RICE BLAST FUNGUS), 608 aa.	3.20E-64	22
3281	cg43917654	360	AAAAATCTACT CTTAATGTATATT [A/gap]TTTCATAT TTGTTTAACAAAA GCAG	A	gap			SILENT-NONCODING	transferase	Human Gene Similar to SWISSPROT-ID:P41819 DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 318 aa.	3.00E-52	5
3282	cg43917654	898	CTCCCTAAGAAC CATAAAAAAAGA T[A/C]ATTTTATT GTTAATTTCATTC CAGT	A	C			SILENT-NONCODING	transferase	Human Gene Similar to SWISSPROT-ID:P41819 DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 318 aa.	3.00E-52	5

3283	cg43936623	112	CATCAACAGAGT TGGGTTTAGGGT T[C/gap]CCCAGG AGAGCAAGGGA GATGGATG	C	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3284	cg43936623	292	TTAAACAGTCAC CACCTGGTACAG T[G/T]TTACAAAA TGGGGAGAGTG ACCACA	G	T			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3285	cg43936623	977	ACTGTGGGAGG CAGGGTTGTGTG TG[C/gap]ATCCG CTGAAATTACCC TTGGCTTA	C	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3286	cg43919796	4264	CACTGTATTTTTG GCGCATGTTGGT G[G/gap]CCCTCT GTGCCCTAGATA TATGCAC	G	gap			SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) (MIP) - HOMO SAPIENS (HUMAN), 890 aa. [pcls:SWISSPROT-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	5
3287	cg43998978	5306	TCCTTGGGGCTG CAGTTTTGTGGT T[gap/A]GAGGGG CCTGGAGAAAAT CATTTTC	gap	A			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3288	cg43998978	5412	CCAGGCACTCAA AAGCTGGGAACC A[G/C]GATCTCAG CGCCAGGTCTAC CAGTT	G	C			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16

3289	cg43998978	5413	CAGGCACTCAAAAGCTGGGAACCAG[G/C]ATCTCAGCGCCAGGTCTACCAGTTC	G	C			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3290	cg43998978	5426	GCTGGGAACCAGGATCTCAGCGCCA[G/C]GTCTACCAGTTCTCGTTTTGGGCCA	G	C			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3291	cg43998978	5427	CTGGGAACCAGGATCTCAGCGCCAG[G/C]TCTACCAGTTCTCGTTTTGGGCCAG	G	C			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3292	cg43998978	5794	AGTCCTAGCAGAAAAATGTGTTAGG[G/gap]GCCTGGCCCAAAGCAGTGTTGGTTG	G	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3293	cg43998978	5795	GTCCTAGCAGAAAAATGTGTTAGGG[G/gap]CCTGGCCCAAAGCAGTGTTGGTTGC	G	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3294	cg43998978	5953	CTCCCAAGTATTACCAGTGGGTACC[A/gap]AAAAAAATGTCCCCTTGAGTCTTTT	A	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3295	cg43998978	5960	GTATTACCAGTGGGTACCAAAAAAA[A/gap]TGTCCCCTTGAGTCTTTTCCTTGTT	A	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16

3296	cg43998978	6126	TTGAATATCAAT GATTTTTTTTTTT[T/gap]TAAGTACT GTTCCGGGGAG AAAAAC	T	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3297	cg43998978	6127	TGAATATCAATG ATTTTTTTTTTTT[T/gap]AAGTACTG TTCCGGGGAGAA AAACA	T	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3298	cg43998978	6306	AGCAGCATCTTT TAAAGCCTGTTC T[T/C]TAAGGTGT CTCGTTAGAGCC CAAAG	T	C			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3299	cg42684254	2485	CCATATATTTTCT GAGTAGCATATA[T/G]AATTTTATTG CTGGAATCTACT AGA	T	G			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P31645 SODIUM-DEPENDENT SEROTONIN TRANSPORTER (5HT TRANSPORTER) (5HTT) - HOMO SAPIENS (HUMAN), 630 aa.	0	17 (17q11.1)
3300	cg40351913	3767	TTCTGGGGAGG GACACAGAGGA CAG[T/C]TTCCCC ATCGCCTTCTGG TTGTTGA	T	C			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
3301	cg40351913	3786	GGACAGTTTCCC CATCGCCTTCTG G[T/C]TGTTGAAG ACAGCACAGAGA GCGGC	T	C			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
3302	cg40351913	3789	CAGTTTCCCCAT CGCCTTCTGGTT G[T/C]TGAAGACA GCACAGAGAGC GGCTTC	T	C			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)

3303	cg43935986	2512	GCCAGATAGCTG TTCCTGAGTTGC A[A/G]GCACGAT GGAGATTTGGAC ACTGTG	A	G			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3304	cg43935986	2553	GGACACTGTGTG CTTTTGGTGGGG T[G/A]GAGAGGT GGGGTGGGGTG GGGTGTG	G	A			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3305	cg43935986	2697	TATTTTAAAATAT TTTCCTTCTTAC[G/A]TGAACTGTA TACATTCATATA GAAA	G	A			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3306	cg43934544	221	GGGCCACAGGC CCCTGCTCCGG CCG[C/T]CGCTT GCAGACCGCGG GCGCCGATG	C	T			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P48029 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1 (CT1) - HOMO SAPIENS (HUMAN), 635 aa.	0	X
3307	cg43935086	2211	TACTTTTTAATGA CTCTGGAATCTG[gap/C]GTAGGCT CGAGCGGTTCC CAAGGCG	gap	C			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0	X
3308	cg43935086	29	TTTTTTTTTTTTT TTTTTTTTTTT[G /T]GGAATGTATG ATTTTTTTAATAA AA	G	T			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0.00E+00	X
3309	cg43935086	30	TTTTTTTTTTTTT TTTTTTTTTTG[G/T]GAATGTATG ATTTTTTTAATAA AAC	G	T			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0.00E+00	X

3310	cg43934534	1405	GTCCCCGCAGG CCCACCACCCTC AC[G/C]CAGCCC CAGCCCTCCAGC CTCTGTC	G	C			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P48029 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1 (CT1) - HOMO SAPIENS (HUMAN), 635 aa.	7.50E-294	
3311	cg43964039	1018	CTCTTCTCATGG TAATAGTGTGGC C[C/A]TCAGTGCA AAGGAGACTAGA ACCCG	C	A			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3312	cg43964039	494	ATTTACTTCACAT TCAAAATAATGC[gap/G]ATTTCAAG CCTGAGCATCAC GGCTG	gap	G			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3313	cg43964039	778	CCCTCAATCCAC AAGCATTTCAAA A[T/C]CTTTTTC TAAAAACCAGCC ATTTA	T	C			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3314	cg43964039	864	TATTTACAAGTT GGCTTGTCCAGA T[A/T]TACTATAA CTTAGTGTCTGT ATTTA	A	T			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3315	cg43992017	206	CCTGAGCTTCCT GCTTAGGGGCC GG[C/gap]CCCCA CCCACAGGGTCT CCCTGGAC	C	gap			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.40E-241	
3316	cg44026704	172	CCTTCTGCTGGC CAGTCTGGGCAC C[T/A]GCAGGCC CCTGAGGGAGG GAGCTGT	T	A			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q99808 EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 456 aa.	1.50E-240	6

3317	cg43920728	85	CCATTTTCCACT AACAAAATAATTT [A/gap]GGATGAA GAATTCTGACTC AGTGTC	A	gap			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)
3318	cg43317499	220	CTGCCTCAGCCA CCTGAGTAGCTG G[C/G]AAGACAG AGCATAACCTTC GGTGGC	C	G			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q90406 TRANSMEMBRANE TRANSPORTER - DISCOPYGE OMMATA (ELECTRIC RAY), 724 aa.	1.20E-231	15
3319	cg39377146	4180	TGTCAAGTCCGT TCCGAAGGCATT T[G/T]CCACTAGT TTTTGGACTATG TAAAC	G	T			SILENT-NONCODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	1.60E-225	
3320	cg44003311	766	TCACGTCCGAGC TGCCCAGGCAGT C[C/T]TTCTGCGC CCTCTGCTGGCC AGATG	C	T			SILENT-NONCODING	transport	Human Gene TREMBLNEW-ID:G2921449 ORGANIC CATION TRANSPORTER-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 424 aa.	1.50E-217	
3321	cg44011204	229	CACACACACA CACACACACA C[A/gap]CACACG TGCACACACACA TCCCCCC	A	gap			SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	

3322	cg44011204	234	CACACACACA CACACACACA C[gap/A]GTGCAC ACACACATCCCC CCACAAC	gap	A		SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3323	cg44011204	234	CACACACACA CACACACACA C[gap/A]GTGCAC ACACACATCCCC CCACAAC	gap	A		SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3324	cg44011204	59	ATAGTTGACACT CAATTTTATTGCT [A/gap]AAAAAAA TGTCCTCTGGAG TGACA	A	gap		SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	

3325	cg44011204	531	ATCTCCTGTCCT GGAGGGTGCTG GG[G/gap]CCCCT GGCTCCCCAGA GTGTGCAGG	G	gap			SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3326	cg44011204	67	CACTCAATTTTAT TGCTAAAAAAA[A/gap]TGTCCTCT GGAGTGACAGC AGGTAT	A	gap			SILENT-NONCODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3327	cg43988801	1574	CAAAAGTTTGGC CACTTCCCTCTC A[A/G]AGACTAAC CCAGAAGGGAAT AAGAT	A	G			SILENT-NONCODING	transport	Human Gene TREMBLNEW-ID:E1283177 ABC TRANSPORTER - RATTUS NORVEGICUS (RAT), 565 aa.	9.80E-195	
3328	cg44025532	1782	CCTGCTGGCCA GGCAAGGGGCC AGA[C/gap]CCCC CCCCAACCCCCA GCTGCCATC	C	gap			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.80E-174	
3329	cg44025532	1790	CCAGGCAAGGG GCCAGACCCCC CCC[C/gap]AACC CCCAGCTGCCAT CGCTCTCCC	C	gap			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.80E-174	

3330	cg43924839	176	TGAAGAAATGTG TATCATCTAACA G[C/A]AAAGAAAT ATGAACCAGATA ATGAA	C	A			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
3331	cg43924839	526	CCTTGTTACTTG AGTATTGTAGCC T[C/T]ACCATGAT TTTTTTTAACACC GTAT	C	T			SILENT-NONCODING	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
3332	cg42328251	238	ACACACACACAC ACACACACACAC A[gap/C]GACAAA ACCACAGGGCTA AGACACA	gap	C			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P97511 ZINC TRANSPORTER - MUS MUSCULUS (MOUSE), 341 aa.	6.40E-146	2
3333	cg43928832	363	TTTTTTTTTTTT TTTTTTTTTTTT[A /T]AGTATTTAAAG AGATTTATTAAAT C	A	T			SILENT-NONCODING	transport	Human Gene Homologous to SWISSPROT-ID:Q15012 GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	2.00E-126	2
3334	cg44930322	977	CTTTTGTTTATTA GCACCAATTTCT[C/T]GCCACTAAG CTATTTGTTTTAT TAT	C	T			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	4.80E-113	
3335	cg43924433	226	TCAATACCTTCA TTACATTTATAAA [T/A]ACAAGATTT ACACAGCACCCC ATCA	T	A			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3336	cg43924433	251	TACAAGATTTAC ACAGCACCCCAT C[A/gap]AAAAAA AAAATTAAAACC CTTTACA	A	gap			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9

3337	cg43924433	261	ACACAGCACCCC ATCAAAAAAAAA A[A/gap]TTAAAAC CCTTTACAAATAT CTACA	A	gap			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3338	cg43924433	261	CACAGCACCCCA TCAAAAAAAAAA A[gap/A]TTAAAAC CCTTTACAAATAT CTACA	gap	A			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3339	cg43924433	261	CACAGCACCCCA TCAAAAAAAAAA A[gap/A]TTAAAAC CCTTTACAAATAT CTACA	gap	A			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3340	cg43924433	334	TTCAAAGGGGTG CTCTGTTAAAGG T[G/C]GGCCCTA GTTAATGGTCCA TTTACT	G	C			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3341	cg43924433	339	AGGGGTGCTCT GTTAAAGGTGGG CC[C/gap]TAGTT AATGGTCCATTT ACTGGTGC	C	gap			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3342	cg43924433	569	TGCATACTCAGA GCAGTTAAGGCA G[G/T]AGTGTGAT GGATGAGAAAAA CTTTG	G	T			SILENT-NONCODING	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3343	cg43961977	149	AACATTCCACCA AAAATCATGACT A[T/C]GCATCTAA CAGCTTCAAAAT ATAGA	T	C			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:Q07837 NA+-INDEPENDENT NEUTRAL AND BASIC AMINO ACID TRANSPORT PROTEIN - HOMO SAPIENS (HUMAN), 685 aa.	5.90E-75	2

3344	cg2986272	1143	ACCTCAGCGAG GGCAACGCGAG CTG[T/G]CCGGA GCCCCCCGCCC CGGAGCCCG	T	G			SILENT-NONCODING	transport	Human Gene Similar to SWISSPROT-ID:O08726 GALANIN RECEPTOR TYPE 2 (GAL2-R) (GALR2) - RATTUS NORVEGICUS (RAT), 372 aa.	3.60E-62	
3345	cg43319894	250	TGCTTCAGAGAT CCCTGCTGGCTC C[A/T]CGAGCAC CCTGGCCCGCA AAGAAGC	A	T			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3346	cg43319894	273	CCACGAGCACC CTGGCCCGCAAA GA[A/G]GCTGGG GGACGTCGGAA GCGAGTCG	A	G			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3347	cg43319894	297	AAGCTGGGGGA CGTCGGAAGCG AGT[C/A]GAATTT GTGACATTTGCA CCAGCAC	C	A			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3348	cg43319894	315	AGCGAGTCGAAT TTGTGACATTTG C[A/G]CCAGCAC CCCCAGCCCAG GAGCCTG	A	G			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3349	cg43319894	366	AGGAGCCTGTAG GGGCCCCGGCT GT[A/G]CAGTCCA TCCTGGTAGCAG GTGAGG	A	G			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3350	cg43319894	378	GGGCCCCGGCT GTACAGTCCATC CT[G/T]GTAGCAG GTGAGGAGGAC ATCCGCT	G	T			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11

3351	cg43319894	381	CCCCGGCTGTAC AGTCCATCCTGG T[A/G]GCAGGTG AGGAGGACATCC GCTGGG	A	G			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3352	cg43319894	387	CTGTACAGTCCA TCCTGGTAGCAG G[T/C]GAGGAGG ACATCCGCTGGG TGTGCG	T	C			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3353	cg43319894	411	GTGAGGAGGAC ATCCGCTGGGTG TG[C/T]GAGGAC ATGGGGCTGAA GGACCCAG	C	T			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3354	cg43319894	834	TGAAACGGCTGT GGGAGGCTGGG CC[C/gap]TGGGA CGCCCTCTCATA GCGTCCAG	C	gap			SILENT-NONCODING	transport	Human Gene Similar to SPTREMBL-ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3355	cg43941204	1662	CACTTTCCATTT CTGCGCCTTTTC T[C/G]TCACCCG GGTGGCGCTGG AAGTTAT	C	G			SILENT-NONCODING	transport	Human Gene Similar to SWISSPROT-ID:P09836 REGULATORY PROTEIN UHPC - ESCHERICHIA COLI, 439 aa.	8.40E-57	11
3356	cg43941204	1866	CCCTGTCCTGCC CGCATCCTACCC C[A/gap]TCCCCA CCTGAAGTGAGG CTATCCC	A	gap			SILENT-NONCODING	transport	Human Gene Similar to SWISSPROT-ID:P09836 REGULATORY PROTEIN UHPC - ESCHERICHIA COLI, 439 aa.	8.40E-57	11
3357	cg43941204	1955	GGTCCTAAGTCC TCTCAGCAGTGG G[T/C]GACTGCT GTTGCCAATACC TCAGAC	T	C			SILENT-NONCODING	transport	Human Gene Similar to SWISSPROT-ID:P09836 REGULATORY PROTEIN UHPC - ESCHERICHIA COLI, 439 aa.	8.40E-57	11

3358	cg43990999	1607	TATTGAATCTGG GTTCTTTTTTGAC [gap/T]TTTTTTTTT TTCCCAATCCAA CAGCA	gap	T			SILENT-NONCODING	transport	Human Gene Similar to SWISSPROT-ID:P32802 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 667 aa.	7.50E-55	10
3359	cg43269525	1024	TCTGTCTGGAAC TTCTGACAATCT G[G/C]CATGACA ATGAGGGTGGG CATGATT	G	C			SILENT-NONCODING	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN--PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.50E-163	15
3360	cg43291895	1030	GTTGTTTCGTTTT GGCTTTTTCTCC[C/T]TCCCCATGT CTGTTCTGGGTT TTCA	C	T			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 238 aa.	3.50E-129	
3361	cg43291895	1075	TTTTCACGTGCT TCAGAGAAGAGG G[G/gap]CTGCCC CACCGCCACTCA CGTCACT	G	gap			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	

3362	cg43291895	1182	AGGGGAGCTGA GCCCGACTTCTA CC[G/gap]GGGTC CCCCAGCTTCCG GACTGGCC	G	gap			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3363	cg43291895	1185	GGAGCTGAGCC CGACTTCTACCG GG[G/gap]TCCCC CAGCTTCCGGAC TGGCCGCA	G	gap			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3364	cg43291895	1230	GCCGCACCCCG GAGGAGCCACG GGG[G/gap]CGCT GCTGGGAACGT GGGCGGGGGG	G	gap			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3365	cg43291895	1262	TGGGAACGTGG GCGGGGGGCCG TTT[C/T]CTGACA CTACCAGCCTGG GAGGCCC	C	T			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	

3366	cg43291895	1304	GGGAGGCCCAG GTGTAGCGGTCC GA[G/gap]GGGCC CGGTCCTGCCTG TCAGCTCC	G	gap			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3367	cg43291895	1354	CAGGTCCTGGA GCCACGTCCAG CAC[A/T]GAGTG GACGGATTCACC GTGGCCGA	A	T			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3368	cg44003015	265	TTTTTTTTTTTTT TTTTTTTTTTTT[G /T]CCTTCAGGAG CATGTTTATTGT GTT	G	T			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P52483 UBIQUITIN-CONJUGATING ENZYME E2-23 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - MUS MUSCULUS (MOUSE), 207 aa.	1.10E-109	
3369	cg44003015	318	AGATGATACATC AGGTGCTCTCTG A[G/gap]CTACAA AGGGTAAAAGGA AATCCTC	G	gap			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P52483 UBIQUITIN-CONJUGATING ENZYME E2-23 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - MUS MUSCULUS (MOUSE), 207 aa.	1.10E-109	
3370	cg44005525	725	CAGCTCTCTTCT GTGACAGACAAA T[C/A]ATGTAAGA ACTGTGAAACCC CAGTT	C	A			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

3371	cg44005525	735	CTGTGACAGACA AATCATGTAAGA A[C/T]TGTGAAAC CCCAGTTTATGT AGCGT	C	T			SILENT-NONCODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
3372	cg44923887	1328	GGGCTGGGCTG GCTGCTCTGGAG GA[G/A]GGGGTC AGCAGGGGCCC AGGCGACC	G	A			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3373	cg44923887	2326	AAGCGAACGCCA GGCGGTGGCAC GT[G/A]TCAATTT CCACAGAGTCCT GCTTTG	G	A			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3374	cg44923887	2367	TCCTGCTTTGCG GGGTGTCTGAAT G[C/T]ACTGCAC GGGGTCTCTGCT CACACT	C	T			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22

3375	cg44923887	2413	ACACTTGCTGGA ACCAATCGTGGC A[G/C]ATTTTAGT CCACAGGTCGCT TTTCC	G	C			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3376	cg44923887	836	TGAACAATGTTA GGCTGCCGAAC CT[G/A]CCCATCA CTCCCCACTTCT GCACAG	G	A			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3377	cg43916797	310	AAGGCCAAAGGT TGAAGGGGTAG GG[A/T]GATGTAA AAGAGTTGGGAA CAAAGC	A	T			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:P51669 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE),, 147 aa.|pdb:SWISSPROT-ID:P51669 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 147 aa.	5.20E-80	5

3378	cg4393935	1049	CAGTAAAATAAA CTGTACAAAGGC A[T/A]TTTAGAAT AACAAAAAATATT TTAC	T	A		SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.|pdb:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12
3379	cg4393935	1050	AGTAAAATAAAC TGTACAAAGGCA T[T/A]TTAGAATA ACAAAAAATATTT TACT	T	A		SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.|pdb:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12
3380	cg4393935	236	CAAGAGACAAGG TTGCAACCCGAA G[G/gap]TTAACA TTTATGTATTTAT GACTGG	G	gap		SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.|pdb:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12

3381	cg43094404	4004	TCCACAACTAAT ATAGACAACTTT A[C/T]GCGTGCG TAAGAGTTTTAC ATGGCA	C	T			SILENT-NONCODING	ubiquitin	Human Gene Similar to SPTREMBL-ID:O08759 E6-AP UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 885 aa.	3.20E-73	4
3382	cg43974851	1140	GCGGGCTCCTCT TCTCATCCATGT C[C/gap]TTTCAG GTCTCAGCGTTT GCTCGCT	C	gap			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1
3383	cg43974851	162	CAGAACACTTTA TGGTTTCAAATC C[T/gap]TTTTTTT TTTTTACCCCAA AGGAAA	T	gap			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1
3384	cg43974851	174	TGGTTTCAAATC CTTTTTTTTTTT[T/gap]ACCCCAAA GGAAATTTGAGA ATTCA	T	gap			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1

3385	cg43947722	336	TACAATTAAAATA AAATAAGCATTT[T/G]TATGATTTTT ACAAATATTGTTT AT	T	G		SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.|pdb:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	
3386	cg43947722	769	GAGTGAAGTAAT CACATGCTAGAA C[A/T]TCAGGGC CAATTGGAAAGT CATTAT	A	T		SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.|pdb:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	

3387	cg43947722	780	TCACATGCTAGAACATCAGGGCCAA[T/C]TGGAAAGTCATTATGAACACTTGCA	T	C			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSNEW-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.|pcls:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	
3388	cg43948669	1717	GGGAAGCAGCGCCGGAGCGGGCGAG[T/gap]TCACGCTTCGGCCCCGCCGCTCTCC	T	gap			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P55854 UBIQUITIN-LIKE PROTEIN SMT3A - HOMO SAPIENS (HUMAN), 103 aa.	5.10E-50	21
3389	cg43948669	1718	GGAAGCAGCGCCGGAGCGGGCGAGT[T/gap]CACGCTTCGGCCCCGCCGCTCTCCC	T	gap			SILENT-NONCODING	ubiquitin	Human Gene Similar to SWISSPROT-ID:P55854 UBIQUITIN-LIKE PROTEIN SMT3A - HOMO SAPIENS (HUMAN), 103 aa.	5.10E-50	21
3390	cg42940644	112	CTTCTTGAAGGTGCAGGCCTTGGAC[C/G]TGCCCAGACTCACAGTCCTGGCTGC	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1

3391	cg42940644	323	GTGACCCTCAGAAATCACAAGGGAG[C/T]GGAGAGAGCTGTGTTCAACATGAAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1
3392	cg42940644	327	CCCTCAGAAATCACAAGGGAGCGGA[G/A]AGAGCTGTGTTCAACATGAAACGCT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1
3393	cg43297012	2231	CTACGTTAACTTTGCCTAGTAGAGG[gap/C]CCTTCTTTGCACTTGCTTCTCATTT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P48382 DNA BINDING PROTEIN RFX5 - Homo sapiens (Human), 616 aa.	0.00E+00	1
3394	cg43917756	277	TTCCCCAAGCCACGCAGGCCATGGC[C/gap]TCAGCTCAGCAGGCTCTCCTCAGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0.00E+00	1
3395	cg43920218	5687	AGTCCTTAAAACAGCAGGAAAGGTG[G/A]GCCTGTCCCCCTTTTGTGCAGCTAC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3396	cg43920218	5756	CTGGGCCTCATTCCTCCAAGTCCAC[G/T]GGAGGGTCCAGAAGAGGGAGTCAGA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3397	cg43920218	6123	GACACTGCTGGCGGGGGCTCAGTGA[G/gap]CACTACTCACAGATCCACACCTGAC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1

3398	cg43920218	6174	CCTGTTGGGTCG AGTCAGGCTGG GC[C/gap]TTGGT CTGCACTGTAGC ACCTGTGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3399	cg43920218	6229	TGAGTTCACATC ATGAATGTGGTG A[C/T]TTCCCAGA TACCATCTCAGG CTTAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3400	cg43920218	6523	GTATAAATATAT GATATAGATTTAT [A/T]TATGTTGTA ACGCCATATATT GAAG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3401	cg43920218	6539	TAGATTTATATAT GTTGTAACGCCA [T/C]ATATTGAAG GCCAACATAACT GGTG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3402	cg43920218	6592	CAGGGTGGGTG ACAGAAAATGAA AG[C/T]CTTTTTG GTGATTGTTAAA GCAAGA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3403	cg43920218	6609	AATGAAAGCCTT TTTGGTGATTGT T[A/T]AAGCAAGA TGTGTATAAAGA AATAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3404	cg43920218	6616	GCCTTTTTGGTG ATTGTTAAAGCA A[G/A]ATGTGTAT AAAGAAATAAAT AGTTT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1

3405	cg43921252	154	CTCCTCCACGGT GGGTGCCAGCA GG[C/gap]TCTCC CCTTTCCAGTGA CCTCCCTC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3406	cg43921252	607	ATGTCACAGGGT CCCCGGGGTGG GG[G/gap]CAGCA GCCAGGGCAGA AAAGCAGAA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3407	cg43921266	915	TTATTTTTCTTTG GCTTCAAGCCCC [C/gap]TCCCATG ACGTGCAGGGC AGGGGGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3408	cg43921266	924	TTTGGCTTCAAG CCCCCTCCCATG A[C/G]GTGCAGG GCAGGGGGTGG GCATGAG	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3409	cg43921266	102	GAAATGGGGAG GCAAGGGCTCTT TA[gap/A]GCGTT TGCCAAAACCAC TGCCACAC	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3410	cg43921266	984	ACGCAGGAAGC CTCCACCCCCAC CC[C/gap]TGCCT GGCAGGTCCCA GATTACATG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3411	cg43921266	118	GGCTCTTTAGCG TTTGCCAAAACC A[gap/A]CTGCCA CACCCCTCCACC CCCTCTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

3412	cg43921266	168	TGCCTTCCTCCT CCACGGTGGGT GC[C/gap]AGCAG GCTCTCCCCTTT CCAGTGAC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3413	cg43921266	482	TAGTGGAATCAC AGCAGGCCAAG CC[C/gap]AGGGG CCCGGCTCAAG CTGTCCTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3414	cg43921266	628	ATGTCACAGGGT CCCCGGGGTGG GG[G/gap]CAGCA GCCAGGGCAGA AAAGCAGAA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3415	cg43921266	654	CAGCAGCCAGG GCAGAAAAGCAG AA[G/gap]CTAGC CTCTATAAAAGC ACCCCTTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3416	cg43921266	805	GAGATAGATGCT TTTTTTTTTTTTT gap/T]GCTTGTGT TTTTCCTTCAGTA TAAA	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3417	cg43921266	866	AAATAACTTCTCT TAGAAAAAAAAA[gap/A]TACAGAAG AAAAAAACCAAA GGGTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3418	cg43921266	911	AGGGTTATTTTT CTTTGGCTTCAA G[C/gap]CCCCTC CCATGACGTGCA GGGCAGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

3419	cg43921289	2069	CCACGTGAGTG GTAGCCGCCGC TGA[G/gap]GCCG AGCCTGCACTGG GGCCACCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3420	cg43921289	2070	CACGTGAGTGGT AGCCGCCGCTG AG[G/gap]CCGAG CCTGCACTGGG GCCACCCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3421	cg43921289	2087	CCGCTGAGGCC GAGCCTGCACTG GG[G/gap]CCACC CAGCCAGGCCT GGGGGCAGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3422	cg43921289	2093	AGGCCGAGCCT GCACTGGGCC ACC[C/gap]AGCC AGGCCTGGGGG CAGCCTCTCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3423	cg43929067	21	CCCCTTTTTTTTT TTTTTTTT[T/A]TGA CTTTCCTACATC AGTTTTATTT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3424	cg43929067	209	ACAAAAGGGACC TGGAATCTGTAA G[G/C]TGATTCCA AAAACGAAATAA GTAGA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3425	cg43929067	22	CCCCTTTTTTTTT TTTTTTTT[T/A]GA CTTTCCTACATC AGTTTTATTTA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

3426	cg43929067	23	CCCCTTTTTTTTTT TTTTTTTTT[G/T]A CTTTCCTACATC AGTTTTATTTAA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3427	cg43929067	24	CCCCTTTTTTTTT TTTTTTTTG[A/T] CTTTCCTACATC AGTTTTATTTAAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3428	cg43929067	25	CCCCTTTTTTTTT TTTTTTTTGA[C/ T]TTTCCTACATC AGTTTTATTTAAA A	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3429	cg43929067	54	CCTACATCAGTT TTATTTAAAACAC [A/T]AACAAGTAT TTCTCTTTCTGTA AGG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3430	cg43929790	189	AAGTACAGCAGC CAACATCTGGTC T[C/gap]AGAGCT GCTGGGAAAAG GGGCAGGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12839 (H326) - HOMO SAPIENS (HUMAN), 597 aa.	0	1
3431	cg43932517	138	CTTTCCTACTGG CGCCGGCTCCT GC[C/gap]AGAGG TCGGGGTGACA GCAGGATCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14746 LDLC PROTEIN - Homo sapiens (Human), 738 aa.	0	1
3432	cg43932517	80	GGTTGTTGTTTT TTTTTTTTTTTTT[T/A]TGGGAGACA CTTCTTTTATTTA GGA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14746 LDLC PROTEIN - Homo sapiens (Human), 738 aa.	0	1

3433	cg43935021	1881	TCCTCTGACTTT TACGGAGGGCTT G[C/gap]CAAAGT AGCCTATTGCAG CCAAAGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43308 KIAA0425 - HOMO SAPIENS (HUMAN), 1224 aa.	0	1
3434	cg43935021	1882	CCTCTGACTTTT ACGGAGGGCTT GC[C/gap]AAAGT AGCCTATTGCAG CCAAAGTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43308 KIAA0425 - HOMO SAPIENS (HUMAN), 1224 aa.	0	1
3435	cg43944666	124	GCCCCCAGCAG GAGCACCACCAC GG[C/T]TTAGCAA AGAATCCCAGAC CCCGCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0	1
3436	cg43947011	127	TAGCTCTTTTTTTT TTTTTTTTTTT[G /T]TGGGATAATC TATTTTAATGAAA CT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3437	cg43947011	265	CTGTGGGCTGG AGGTGGGATACC CA[C/gap]CCGCA GCACGCCCACC CTAATGTGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3438	cg43947011	267	GTGGGCTGGAG GTGGGATACCCA CC[C/gap]GCAGC ACGCCCACCCTA ATGTGCCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1

3439	cg43947011	330	GAGAAAGGACA GTGGGAAGGAG ACA[G/gap]TAGG CTCAGCCCCAGAG ATGCCCCCTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3440	cg43948542	4725	ATTAGTATCTTCT CAGATACAGACC [A/G]TTTTATGAT TTTTTAAAAAGTA AAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
3441	cg43948542	4772	AAAAGTTCTAAA ATGAAGTCACAC A[A/G]GACAATTA TTCTTATGCCTA AGTTA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
3442	cg43950151	991	CACACAGTCAAC ACCTTGGTGACA G[G/gap]CATCTG CCCCCACTTCAA CCAGTAA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
3443	cg43950151	2156	ACACGTGCCCCT GGGGGAGCCCA CA[C/T]GGCACTT AGGGCTGGCAG CACCGCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1

3444	cg43950151	273	CGTTTTTTTTTTT TTTTTTTTATGG[A/T]TTTCCAACTA GGTTTTATTTTAG TT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
3445	cg43961075	114	CCTTGAAAACTT CTCATCCCCTGA A[G/gap]GGTGGG GTGACCACCCCT CTGGGAC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa.	0	1
3446	cg43969426	4957	TATTTCATCCAAA TCAAGCTAAAAT[G/T]TATTTAAGTT GATTCTGAGAGT ACA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0	1
3447	cg43970200	270	AGTAGCTTTTCA GCATTCAGTTTT G[A/T]GGCTCATG GGAAATGTTACT TAGCA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0	1
3448	cg43970200	319	CATCAAGATGTG GTTTGATGAGTG A[A/G]CAATGTCA GTATCAACTGTA CTTAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0	1
3449	cg43994728	1881	CAGGAATTTAAA ACCAAGGATAAG A[G/T]ATGCCTTT GTCAAATCTTGG TTCCA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75041 KIAA0453 PROTEIN - HOMO SAPIENS (HUMAN), 1052 aa (fragment).	0	1
3450	cg43994728	2157	AACAGTTCAATG GGACTTTTTTTTT [gap/T]CCTTCTCA ATCAACAGAGTT TACCA	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75041 KIAA0453 PROTEIN - HOMO SAPIENS (HUMAN), 1052 aa (fragment).	0	1

3451	cg44020180	1972	TTGTAGCAGAGA CACAGTGGCCTA G[C/gap]CAATCG GCAGTGCTATAC ACACAGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0	1
3452	cg43925699	2081	TTGTTATAAGGC GCTGGGAGAGG AT[G/gap]GGCAG CTCCCACTGCCC CAGAGCGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
3453	cg43925699	2083	GTTATAAGGCGC TGGGAGAGGAT GG[G/gap]CAGCT CCCACTGCCCCA GAGCGGAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
3454	cg43926985	4868	CAGCATGTCCCA GTCACTGCAGCA A[C/T]GCCTTGTG TTTGTTTCATTTT TTTA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
3455	cg43926985	5521	GTATAAATTAGA AAATGAAAAATG T[G/A]TGAATAAC ATTGTATGAAAT AAACC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
3456	cg43961763	115	TTTTTGGTCCAG TACTCCACAAAA C[A/G]CTACAGAC AGTAACAAAATA ATTCA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOGRANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0	2
3457	cg44033553	635	TCATGCCTGAGA CCAGAATGGAAT A[G/A]AACAATCC ATTTGAATACAG CGATG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42331 HYPOTHETICAL PROTEIN KIAA0053 - Homo sapiens (Human), 638 aa.	0	2

3458	cg44911887	144	CCGAGGCCTCCTTGCTTCCCGCTCT[G/C]CGAGGAGCCTTTCATCCGAAGGCGG	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3459	cg44911887	165	CTCTGCGAGGAGCCTTTCATCCGAA[G/gap]GCGGGACGATGCCGGATAATCGGCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3460	cg44911887	96	GAGCTTGGCCGGTTTCGAGTCGCTG[A/G]CCTGCAGCTTCCCTGTGGTTTCCCG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3461	cg44927137	3131	ATTTTGGTGTGCTACAAAAGCCTTT[A/G]CAAATTATCAGTAGTAGTTTTTTTT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
3462	cg44927137	3449	TTTGTCTATAAATGGAGCTGTTTAT[G/A]GCAATTTAATACCATTCTCTTTGTA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
3463	cg43301812	1497	ATGGACAATGAGTGCTCCTCTGCAC[C/T]CCCCCATATCAATGGCAGTGGAACC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
3464	cg43308354	1161	CACCTAGTCCTCTGCTACCAACTCA[T/C]GTCATGATGGGGATGAGCCAGACAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3

3465	cg43308354	1382	CAATGGTGTTGT TAGACTCCCCTA T[T/gap]TTTTAAA ATGCTAATTCAC ATTCTT	T	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3466	cg43308354	300	GACAGAACAATC AAAGACCAACGT G[C/gap]ACCTTG CTTTCCATACCA GGCTGAG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3467	cg43308354	436	CTGTGGGGAGA GGGTAGGCAAT GGC[C/gap]TCCT GCAAACGGGCC CAGATCCGCC	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3468	cg43308354	90	ATAATACAGCAA GATATTGTTGGG G[G/T]TTTCTTTT TTTCTGTCAAGT AAGAA	G	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3469	cg43918935	3056	CTGTGTTTATCA TGTGTATATCGT C[C/T]AGAAAGTA TTAAGGCTTTAG GTAGA	C	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
3470	cg43925942	4379	AAATACTTCCGA AACCAGGAATTC A[G/A]TGTATGTT TGTTTTATACTGT TTGA	G	A		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3471	cg43925942	5380	GCTATAGTTGCG GGTGGAACAGTC A[A/G]CCTTTCTA GTAGTTTATGAT ATTGC	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3

3472	cg43925942	5427	TTGCCCTCTTTG TATTCCCATTTTC [T/C]ACAGTTTTT TCCGCAGACTTC TTTC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3473	cg43925942	5713	ATGGTTTTTCTCT CAGTTCTCTAAG[C/T]TGGTCTATG TTATAGCTCTAG CAGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3474	cg43925942	5909	ATTATTGCAACTT ATATTTTGCCTG[A/T]GCTTGATCA AAGGTCATTTGT GTAG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3475	cg43925942	5964	GTAATTAAAAAAT ATTTAAATCACA[A/T]TAAAATTCTA TTATTGGAGAGC ATC	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3476	cg43925942	5967	ATTAAAAAATATT TAAATCACAATA[A/T]AATTCTATTA TTGGAGAGCATC TTT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3477	cg43936625	38	TTTTTTTTTTTTT TTTTTTTTTTTT[A /T]TACTAAAAGAA TAAAGATTTTTAT T	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14688 KIAA0183 PROTEIN - HOMO SAPIENS (HUMAN), 1062 aa (fragment).	0	3
3478	cg43939697	3385	TAAATGTTTTTG GCCGGGCGTGG TG[G/gap]CTCAT GCCTGTAATCTC AGTACATT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3

3479	cg43940975	130	TCTTTTTTTTTTTTT TTTTTTTTCTA[G/T]GAGAATTTA GCTGTTCTTTATT GAC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
3480	cg43940975	131	CTTTTTTTTTTTTT TTTTTTTTCTAG[G/T]AGAATTTAG CTGTTCTTTATTG ACA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
3481	cg43957007	2507	AGTGATCCTTCT GCCTCAGCCTCC C[A/G]AGTAGCT GGGATTACAGGT GAGCAC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92611 MYELOBLAST KIAA0212 - HOMO SAPIENS (HUMAN), 657 aa.	0	3
3482	cg43979396	6657	AAAGGAGAGG GGTTAAGATGCA CC[G/A]AGGCTG TAGCTGGGCTAC TTGATCT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA31595 KIAA0620 PROTEIN - HOMO SAPIENS (HUMAN), 1985 aa (fragment).	0	3
3483	cg43979396	6750	AGCTTTTATATAT TAAAAACGTAT[C/T]ATGCACCAA CTGTGAATAGCT GCCG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA31595 KIAA0620 PROTEIN - HOMO SAPIENS (HUMAN), 1985 aa (fragment).	0	3
3484	cg44021891	466	TGGTAATACTGA GGGGCTGGACA GA[G/gap]GCTCT TCTGAGCCTCAA GCGCCAGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
3485	cg44021891	479	GGGCTGGACAG AGGCTCTTCTGA GC[C/gap]TCAAG CGCCAGGGACA GAGACCTAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3

3486	cg43917191	1115	CTATATGGAGTA AAATAAGTTAAA A[C/T]TTTTCTAA TGAGAATAGCTG ACAGG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
3487	cg43917191	1120	TGGAGTAAAATA AGTTAAAACTTTT [C/T]TAATGAGAA TAGCTGACAGGC AGCA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
3488	cg43918628	3240	GTGTGTGTGTAT ATATATATATATA [T/gap]AATACATT CTATCTTACCCT AATCA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3489	cg43918628	3241	TGTGTGTGTATA TATATATATATAT [A/gap]ATACATTC TATCTTACCCTA ATCAT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3490	cg43918628	387	ACAAAATCTAAA AAGAAAACAAAG C[gap/A]AAAAAA AAAAACCCCTT CATATTC	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3491	cg43926426	5172	TGTACATATCTG GGCCTTTGGAG GC[C/gap]ACGTG TGGCATGGGAG GGGCTACCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75338 RGS12 - HOMO SAPIENS (HUMAN), 1376 aa.	0	4
3492	cg43930961	1361	CAAGCCAGGTCT TCCCGTCTTCTT G[G/gap]TGTGGC CACACCCTGTCC GGCATAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4

3493	cg43930961	26	TTTTTTTTTTTTTTT TTATAGGCAAGG [C/T]TTTATGTTA TATTTATTTATTT TCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
3494	cg43930961	629	AAAATCCAAGAC CAGCAGTTCCTC A[C/A]ATTTGAGT ACTACTCAGATT GGCAG	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
3495	cg43935402	14000	GACCACTCACGA TAAAGCAGATTT T[T/gap]CTCTGC CTCTGCCACAAG GTTTCAG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
3496	cg43979400	1082	CACACTTTCATC TCTGTTGCTGAA A[G/gap]CCTCTG AGCTTCAGCTAC TTAACTA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3497	cg43979400	2010	GCACATACTGCT CCTCCTGGCCTC T[G/gap]CCTGTG GCACAATGCCAT GAGAGCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3498	cg43979400	2080	CACAGACGCGA CTCACAAGATGC GC[C/gap]GGCTC CCCGGGCTCAC CAAGGAGAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3499	cg43994452	163	ACTGGCAGGGA CCTCCCCCACAG CC[A/G]CCCCCA CAGGGTTCTCTG TTTCCCA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4

3500	cg43994452	242	ACACATTCACCC ACTACCTGCTGG A[G/C]AGGAGGG TCATGAGGCAGC CTGTGG	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3501	cg43994452	50	TTTTTTTTTTTT TTTTTTTTTTTT[G /T]CAGGTTCCAC CAGAGGCTTTTA TTT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3502	cg43994452	572	TTCCAGACACCG GAACCTCCTAGT C[T/C]AGCCTGG CACACCCATGTC ACTCAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3503	cg43994452	593	AGTCTAGCCTGG CACACCCATGTC A[C/T]TCAGAAAG GTCAGGCTCAG GGTGGA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3504	cg43994452	697	GCAGCCTTCCCT TTGTCGGGGTCC A[T/C]GCAATCTA CACATGGTCGCA AGGTC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3505	cg43994452	772	GGGCACAGACG GCACTGGTGCAT GC[C/gap]TGTCG GGCTGGGGCCA CACTGGGGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3506	cg43260923	908	CACATAATTCCA ATTTTTATTGAAT [G/A]TAGAGATTT TATGAAAACAAA TCCA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15023 KIAA0305 - HOMO SAPIENS (HUMAN), 1539 aa.	0	5

3507	cg43916866	104	TGTGTGCCAGGACAACCGGCCGGAG[C/gap]CACCGCAGCTCCCGATACCGATGTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3508	cg43916866	1412	CCTGTCGAGATCACAGCAGGTCCAA[A/T]ATAAAGTGACAACTAGATTTAATAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3509	cg43916866	1413	CTGTCGAGATCACAGCAGGTCCAAA[A/T]TAAAGTGACAACTAGATTTAATAAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3510	cg43916866	176	AATTGCTTACCACTTAGGGAAAAAA[T/C]TGTTGAAGTATAAAACAGCCAGAAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3511	cg43933355	236	CTGAGACTTAATAAATGAGATAAAA[G/A]CAGTTTCTTACACCTAAGAAACTGG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
3512	cg43933355	42	TTTTTTTTTTTTTTTTTTTTTTTT[T/A]TTCGAACCAAGAGAACATTTTTTAT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
3513	cg43933355	403	CCAGGGGATGCTGGGCTTGTTAGCA[C/T]TCAAGCTCTGGGACCTGATTGGCCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5

3514	cg43934069	304	AGTAAAGATTTC TTTTTGGTGTATA [C/gap]CAGAGTT AAGGGCAGTAGA AGAATA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92585 MYELOBLAST KIAA0200 - HOMO SAPIENS (HUMAN), 1016 aa.	0	5
3515	cg43934069	582	GTCTGAGCACCC TTTTCTTCTGAGT [C/T]GTGGCTCCT GGAAGACGGGG CTGTG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92585 MYELOBLAST KIAA0200 - HOMO SAPIENS (HUMAN), 1016 aa.	0	5
3516	cg43942958	1107	CAAGCAAGGGC AGATCTGAGAGC CT[C/G]TAATGCT AGGCAGGTGCA GCTGGTG	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3517	cg43942958	1353	GGGAGGAAAGG CAGGAGGAGAT GAG[G/gap]CCAG CCCCACTGATGA CACCTTGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3518	cg43942958	1378	GCCAGCCCCACT GATGACACCTTG G[G/gap]CCAGGC CTCACAGCTGCA GGCATCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3519	cg43942958	329	AGTGAGGGTATC CTTGTGGCTCCA G[C/gap]CCTGGG GCCCCCTGCGG TCACCTTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3520	cg43942958	331	TGAGGGTATCCT TGTGGCTCCAGC C[C/gap]TGGGGC CCCCTGCGGTCA CCTTTGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5

3521	cg43951735	319	ATAAATCTTCTCT TAGGCTAAACAA[C/gap]AAGACTCG GTCTATAATTCA GAGGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14776 PUTATIVE TRANSCRIPTION FACTOR CA150 - HOMO SAPIENS (HUMAN), 1098 aa.	0	5
3522	cg43951735	34	TTTTTTTTTTTTT TTTTTTTTTTTT[A /T]TATAAAAAGG GTTGGTTTATTG TAG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14776 PUTATIVE TRANSCRIPTION FACTOR CA150 - HOMO SAPIENS (HUMAN), 1098 aa.	0	5
3523	cg43981461	5659	ATTAAAGAAGTT CATAGATTTCAC A[C/T]GAATGTAA ATGTGTTATATG GAGAC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43314 KIAA0433 - HOMO SAPIENS (HUMAN), 1243 aa.	0	5
3524	cg43985488	443	CACGCCAGGCC CCAAGCAGGGT GAG[G/gap]CCTC CAACCCGGCCA GCTGAGCAGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q16643 DREBRIN E - Homo sapiens (Human), 649 aa.	0	5
3525	cg43985488	711	GAATGCAGGCAC GGCGGGCCGTC TG[G/gap]CCAGA GGCTGATGCAG GTGGGCGGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q16643 DREBRIN E - Homo sapiens (Human), 649 aa.	0	5
3526	cg44026925	5069	CAATGAATCAAG ACTTCTACCCAA A[G/A]CAACATTT TTTTAAACTATAT TTAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3527	cg44026925	5421	AATCAAATTCAA AGATTTAATTCTT [G/C]CTATGAATT CTAAAGTTCGGC AAAC	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5

3528	cg44026925	5450	TGAATTCTAAAG TTCGGCAAACCA A[T/C]TCATCATA AAATCCAAATAA TCTTG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3529	cg44026925	5504	CCTATTTATCTA GTGATTCATCTC C[A/G]ATTCTGTT GAAAAAGCATAA TATAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3530	cg44026925	5525	CTCCAATTCTGT TGAAAAAGCATA A[T/C]ATAAATGT TGATGAGACTAG ACTCT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3531	cg44026925	5536	TTGAAAAAGCAT AATATAAATGTT G[A/G]TGAGACTA GACTCTAATGGA TATGT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3532	cg44026925	5541	AAAGCATAATAT AAATGTTGATGA G[A/T]CTAGACTC TAATGGATATGT TTATA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3533	cg43308181	5595	ATCATTTTCTTTT TTTTTTTTTTTT[T/ gap]CTGTTGTGG AAAAGCGTGAAT TTGT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92514 MYELOBLAST KIAA0240 - HOMO SAPIENS (HUMAN), 983 aa (fragment).	0	6
3534	cg43308181	5912	AAAATGTTTTGTA AAAAAAAAAAAA[A/gap]CTATAACA AATTGCAGTTTA TTTTG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92514 MYELOBLAST KIAA0240 - HOMO SAPIENS (HUMAN), 983 aa (fragment).	0	6

3535	cg43924112	351	AAAATCTGAGAC AAGACTAAACAA A[C/gap]AACAAA AAAATCTCTAAC ACAAAAT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
3536	cg43924112	5634	CGCCGCCCGCC CCGGCCCAAAA GTC[C/gap]GCCC GCGCTGTCCACA CAGTGGGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
3537	cg43925091	168	TTTTTATAATCAA ACTCTTGGGTTT[T/A]ATTTCTGTAA AAGCTCCAGCTC TAC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0	6
3538	cg43929503	327	TTTTGGTTTATAG GAGAGATTTATT[T/A]GAAGAAATA TTACAACATATAA AAA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
3539	cg43929503	430	TAATAAAAAACTT TTAAAATCCAGA[A/T]TGCACAAAG TACTGCACAATT TGAT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
3540	cg43929503	5399	TGTCTCTTTCCA AATCTTTGAGCC G[G/C]CTGCGGA CATCGTCGGGCA GCGAGA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6

3541	cg43947531	101	CAAATTAAACAAGTTTGTTGAACAG[C/A]TTTCTTTTCTAATATAATGACTATG	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14244 MICROTUBULE ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 749 aa.	0	6
3542	cg43998751	2414	GGCTACAGTACCATGCCTCTCAGCC[C/gap]CGTGTGTATAATATGAAGACCAAAT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3543	cg43998751	346	GCGGGGTGGAGCGGCACGCGCCTTC[G/T]GCAGGAGGCTGAGTGTCCGTCTCGC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3544	cg43998751	352	TGGAGCGGCACGCGCCTTCGGCAGG[A/C]GGCTGAGTGTCCGTCTCGCGCCCGG	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3545	cg43999667	395	AACTGTTTTATAACAAACACAAAAT[A/gap]AAAAAAAACAATGTTACTATTTACG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6
3546	cg43999667	403	TATAACAAACACAAAATAAAAAAAA[A/gap]CAATGTTACTATTTACGGCAAACAG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6

3547	cg43944072	282	TTAGTGCGGTAC ATGCAGCCCTCG G[C/gap]ACGGAG GGTCAGTCCCC GCTGTTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60719 CULLIN 1 - HOMO SAPIENS (HUMAN), 776 aa.	0	7
3548	cg44018111	266	ACTCCCAGGACG GGGGCCAGGCC CC[gap/C]TAAAA AGGCACAATGGC AGGGCAGG	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O60568 PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 3 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 3) (LH3) - Homo sapiens (Human), 738 aa.	0	7
3549	cg43316178	2924	GTCCACCACTCT ACCCCACAGGA GG[G/gap]CCGCC CGCCACCAAGC CTCACCTGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14163 KIAA0150 PROTEIN - HOMO SAPIENS (HUMAN), 944 aa (fragment).	0	8
3550	cg43274140	3669	GGTGGGAGAGG GGGAGTCTCAC GGG[G/gap]CCCC AGGCTTATTCAG AACTGGTGT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75151 KIAA0662 PROTEIN - HOMO SAPIENS (HUMAN), 677 aa (fragment).	0	9
3551	cg43274140	3831	CATGTACATTTC TAACAAAGTTTAT [C/T]GTGGCTATT AAAGTGTTTTATT TCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75151 KIAA0662 PROTEIN - HOMO SAPIENS (HUMAN), 677 aa (fragment).	0	9
3552	cg43916922	172	TTACCCAGGCCC ACTGTTCCTATG C[G/A]CACTGGC TTTGTAGGCATT CACATC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75181 KIAA0699 PROTEIN - HOMO SAPIENS (HUMAN), 847 aa (fragment).	0	9

3553	cg43947535	1017	GGCAGCACCCC TCCCAGAGGCA GCC[A/G]GGGAG GCCTCTCCACCA GGGCCTGC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21399 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON REGULATORY PROTEIN 1) (IRP1) (FERRITIN REPRESSOR PROTEIN) (ACONITATE HYDRATASE) (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE) - Homo sapiens (Human), 889 aa.	0	9
3554	cg43958488	241	GTTGAGCACTGG ATTCAGGTAGAG G[A/gap]GGGCTC CCAGGTCAGTCT GAGAGTT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
3555	cg43958488	79	ATTTTCAAAGTC ATTGACCTCTTG T[A/G]TCAGATTT AAGGCAAAGAAG AAGAT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
3556	cg43970044	357	GGTCTCCACCTG AAAACTTCTGCC T[C/T]GGGATTGA CAGCCATCCATA AGAAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75129 KIAA0634 PROTEIN - HOMO SAPIENS (HUMAN), 1321 aa (fragment).	0	9
3557	cg43976962	836	GAGGGTGCTGT GGTCACAGCTCG CG[G/gap]CCCCG GCCACCGAGGC CCAGTTCCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92854 SEMAPHORIN - HOMO SAPIENS (HUMAN), 862 aa.	0	9
3558	cg43976962	842	GCTGTGGTCACA GCTCGCGGCCC CG[G/gap]CCACC GAGGCCCAGTTC CCTTCCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92854 SEMAPHORIN - HOMO SAPIENS (HUMAN), 862 aa.	0	9

3559	cg43251586	1145	TTGATCAACAGT TGACAGTTAGTT G[C/T]GAGGAAA GGGTCCAAAAG GCATGGA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76041 NEBULETTE - HOMO SAPIENS (HUMAN), 1014 aa.	0	10
3560	cg43923753	466	GTCACTTCCTGC AGCCATACCGTC A[G/gap]GCCAGC TTGGCCTAAAAG CTGTTAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
3561	cg43923753	467	TCACTTCCTGCA GCCATACCGTCA G[G/gap]CCAGCT TGGCCTAAAAGC TGTTATC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
3562	cg43925660	124	ATGCCTTGTTTTT TTTTTTTTTTTT[A /T]TGGCTGTTAT GCTTTTAATGGA AGC	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13772 ARA70 - HOMO SAPIENS (HUMAN), 614 aa.	0	10
3563	cg43950416	42	CAGCAGCAGAG GGAGAGCTCGG GGC[G/T]TGAAG GGGAAACAGCG GAAGACCTA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10
3564	cg43950416	4189	AGGTAGGGTTCA GGGACTGATTGG T[C/gap]CCATTT GCCCTCAGGTCA GTTGTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10
3565	cg43950416	4192	TAGGGTTCAGGG ACTGATTGGTCC C[C/gap]ATTTGC CCTCAGGTCAGT TGTTTAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10

3566	cg43917151	113	TGCCAACTCCTG AGCTAGGACCTG G[G/T]AACACAAA GTTAAATAGGAC ACGAT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC98480 LYSOSOMAL PEPSTATIN INSENSITIVE PROTEASE - HOMO SAPIENS (HUMAN), 563 aa.	0	11
3567	cg43983056	1243	CCCACACACGTT AGACAATTTTTTT [C/T]TTTTTTTGC CAAGATTTTAGT AGTA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3568	cg43983056	1313	TACTTTCACTCC TTCAGTGTTAAA A[T/C]AGAAAACC AAACAGTGCCAA CAGTA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3569	cg43983056	2744	CTCTAAGGTACC TCCCATCCCCCC C[C/gap]ACCCCC AAAATCCCGCTG ATTTCTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3570	cg44015570	435	TAAAAAGTAAAA GCCACATCTGCA A[C/gap]TTACAC AATCCAAAATGG CTAGAGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13136 LAR-INTERACTING PROTEIN 1B - HOMO SAPIENS (HUMAN), 1202 aa.	0	11
3571	cg43329920	303	GCAGGGATGCTT AAGGAAGGCCC CG[C/gap]CCAGT ATGAAAGCTGAG GATTGCCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12
3572	cg43329920	305	AGGGATGCTTAA GGAAGGCCCCG CC[C/gap]AGTAT GAAAGCTGAGGA TTGCCTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12

3573	cg43918566	2146	CCAGACTCTTCC TGGACTGGCTTG C[C/gap]TCCTCC CCACCTCCCCAC CCTGGAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3574	cg43918566	2534	AGTCGTTTTACC CTCTTCTATTGA A[T/A]TGCCTTGG GATTTCCTTCTC CCTTT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3575	cg43918566	2581	CTTTCCCTGCCC ACCCTGTCCCCT A[C/A]AATTTGTG CTTCTGAGTTGA GGAGC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3576	cg43918566	2668	CCTATCACCTCC AGCACAATCCCA G[C/T]GAAAAAG GTGTGAAGCACC CACCAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3577	cg43924515	390	ACATGCTTGGTC TTTCTGGCTTGG C[C/gap]AACTCC TTCCTTGAAACT AAGGGCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P29728 (2'-5')OLIGOADENYLATE SYNTHETASE 2 (EC 2.7.7.-) ((2-5')OLIGO(A) SYNTHETASE 2) (2-5A SYNTHETASE 2) (P69/P71) - Homo sapiens (Human), 726 aa.	0	12
3578	cg43932638	175	AGCTGCCGCTG CCACCAGAGCC GGC[G/gap]GGG CATCGCGCTGCT CATTCATCCG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43892 BICAUDAL-D - HOMO SAPIENS (HUMAN), 975 aa.	0	12
3579	cg43950437	295	GAGTAGCTGGG ATTACAGGCGCA CG[gap/C]CAATA CGCCCGGCTAAT TTTTTATT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0	12

3580	cg44918447	227	AATCCCAGCACT TTGGAAGGCTGA G[A/G]CAGGAGG ATCAGTTGAGGC CAGGAG	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3581	cg44918447	239	TTGGAAGGCTGA GACAGGAGGAT CA[G/C]TTGAGG CCAGGAGTTCAA GACCAGC	G	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3582	cg44918447	276	AGTTCAAGACCA GCCTGGGCAAC AT[A/G]GTGAGA GCCTGTCTCTAC AAAAAT	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3583	cg44918447	475	TGAGACCTTGTC TCAAAAAAAAA A[A/gap]AACGC CTCCCCCCTACC CCAGACA	A	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3584	cg43961443	242	AATTATTTTCTTC GAGCCCGCTCT G[C/gap]GCTGCG CCGGCCTCCCC GCGCCCGG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14393 GROWTH-ARREST-SPECIFIC PROTEIN - HOMO SAPIENS (HUMAN), 678 aa.	0	13
3585	cg43966200	530	CTCAATTGTTTATT ATATATTTTTTTT /gap]ACAAGTTTT AACCTTTTGGAA AAAC	T	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13
3586	cg43966200	733	ATTTTTATTCATT TTAAATCAAAGA[G/A]ACCATTCCA TTTCCTAACAAA CAGG	G	A		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13

3587	cg43966200	817	CAGTCTTTCCCT GTTTTGAACAAG T[T/C]TTTTTGAG AATTCTTAGTTTT AGTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13
3588	cg43975253	415	AACAGTAGAGTT GTGCAATATGGA T[G/A]TTTCTTAC TACAAGAAAAAA ATTAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3589	cg43975253	52	TTGGGTGATGCA GAAAGCCACAAA T[T/G]TTAAAAGG ACACTAAGGTTT TAATA	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3590	cg43975253	54	GGGTGATGCAG AAAGCCACAAAT TTT[T/G]AAAAGGA CACTAAGGTTTT AATAAG	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3591	cg43929104	2930	ACAAGAGGAAGT GCCTGCGGGTT CC[T/C]TTTTAG AAGCTTTGTGGG TTGATT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3592	cg43929104	3069	GTCAGTATTTCA GGGTTCTACATT T[T/gap]ATCTGTA AAATGTGACTTT TTTTTT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3593	cg43929104	3086	CTACATTTTATCT GTAAAATGTGAC[T/gap]TTTTTTTTT TTTTATCACAACA GAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14

3594	cg43929104	3098	TGTAAAATGTGA CTTTTTTTTTTTT[T/gap]TATCACAA CAGAAGTAAAAT GTTGC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3595	cg43929104	3099	GTAAAATGTGAC TTTTTTTTTTTTT[T/gap]ATCACAAC AGAAGTAAAATG TTGCT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3596	cg43929104	3099	TAAAATGTGACT TTTTTTTTTTTTT[gap/T]ATCACAAC AGAAGTAAAATG TTGCT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3597	cg43929104	367	AGCGGAGCCGA GTTTGAGGCAGC GC[C/gap]TAGCG GTGAATCGGGG CCCTCACCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3598	cg43929104	3568	CATTTTGATTCT GAAAAGAAAGCT G[G/gap]CTTTGC CCATTTCTTATTA AAAAAA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3599	cg43933104	1960	GCATACTCTGGC AATGTTGTTCTTT [gap/A]AAAAAAG CATGGATTGCAT TTATAT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA31641 KIAA0666 PROTEIN - HOMO SAPIENS (HUMAN), 1085 aa (fragment).	0	14

3600	cg43933104	1966	TCTGGCAATGTTGTTCTTTAAAAAA[gap/A]GCATGGATTGCATTTATATAGTGTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA31641 KIAA0666 PROTEIN - HOMO SAPIENS (HUMAN), 1085 aa (fragment).	0	14
3601	cg43948117	2921	ACCTGTCAAGTGTCAACCCATACCC[T/C]GCAGAAGGCATGGGCTGCCACTCGG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15040 KIAA0329 - HOMO SAPIENS (HUMAN), 1411 aa.	0	14
3602	cg43949523	136	AGCGTGGTGTTCAAAGGCTTTTAGC[C/gap]TCATCTCATATCAGTCTAGTCAGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15035 KIAA0321 - HOMO SAPIENS (HUMAN), 1542 aa (fragment).	0	14
3603	cg43968223	164	GGCATCTCTTAGGCGGGCAGGACGG[C/gap]CCCCCCAGGCTCAACTCAGGACAAC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3604	cg43968223	218	AACGGGACTGAGCGGCCCCATGGCC[C/gap]TCGGCCTGTGGCCACTGAGCTCCGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3605	cg43968223	388	TCCATGGCTCAGCATCGTCCTTCTG[G/gap]CTTCCCAGCCCCGGGCCGAACGTTC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3606	cg43991855	247	GCCTCTAAGTTTAGCCCTGCAACCA[A/gap]AGAGTTCCTCCAGGGAAGGAACGCT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15037 KIAA0323 - HOMO SAPIENS (HUMAN), 724 aa (fragment).	0	14

3607	cg44018598	473	GGCAGTTCTAAA TAGCAAGTGCTT C[C/gap]ACAAAA ATAAAAAAAACG ATAATGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
3608	cg44018598	592	CTATTCAGCTGG GTAATATTTTGAT [gap/T]GTTTATCA TGTGCACTTGCT TGTCT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
3609	cg44022133	4396	TATTATTAAATGA TGTGGTCTATGG [A/gap]AAAAAAAA TAAAAATCTGAC TTAGT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0	14
3610	cg43298473	3230	CAGCAGTTTGCA GTGGGGTAAGG AG[G/gap]CCAAG CCCATTTGTGTA ATCACCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD32135 CYTOSOLIC PHOSPHOLIPASE A2 BETA - HOMO SAPIENS (HUMAN), 1012 aa.	0	15
3611	cg43936094	85	CAACATTTATTTT ATCATAAAAGTT[C/A]AGCAAATAA AACTATATACAA GATC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC62018 P53 TUMOR SUPPRESSOR-BINDING PROTEIN 1 - HOMO SAPIENS (HUMAN), 1972 aa.	0	15
3612	cg43149413	3078	TTTGCCCACGTA CCCAGGTCTGG CT[G/gap]GGGCC CAGGCCCGGAT GCAGAGGCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3613	cg43149413	3101	CTGGGGCCCAG GCCCGGATGCA GAG[G/gap]CCTG CAGGGCCTCTGT CAATTGTAC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16

3614	cg43149413	3135	GCCTCTGTCAAT TGTACGCGCCAC C[G/A]AGTGCCTT CAACACAGCTTG TCTCT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3615	cg43149413	3148	GTACGCGCCAC CGAGTGCCTTCA AC[A/C]CAGCTTG TCTCTTGCCTGC CACTGT	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3616	cg43149413	3277	GTAAATATGTAC ATTTCTCAGGCT A[G/gap]GGCCAG CAGGGGCTGCC CGAGTCTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3617	cg43928515	1062	GTGAAGTAGCTG AACAAAAAACTT A[A/gap]AGAGAT TGCATGTCAATT TTTAAGC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3618	cg43928515	16	TTTTTTTTTTTTT TT[T/C]TTAATTTA GGAAGATTTTAT TTTTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3619	cg43928515	214	CACCGGTGTTCC TCCCTCCCACCT G[C/T]GTATGGG GTTTACTGTTATA GAATT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3620	cg43928515	2886	AACATACAAAAC TTTGTTTTTTTTT[T/gap]AATATATA TACACAGTACAA GGCTG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16

3621	cg43928515	3260	TGGGGAGGAATGAGACTGGCCCCAT[C/T]GCTGCGGCAAAAGCAAACTGGGCTT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3622	cg43928515	3265	AGGAATGAGACTGGCCCCATCGCTG[C/T]GGCAAAAGCAAACTGGGCTTGAGGC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3623	cg43934724	428	AGAGGAATCTAGCGCGTCTGGCAGG[G/gap]CTGCGCTTCTTCACCTGCCCCTTAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15058 KIAA0350 - HOMO SAPIENS (HUMAN), 917 aa (fragment).	0	16
3624	cg43945577	2336	CCAAGAAACAGAAGACAAGGCGGAC[G/T]TGAGGAGGAAGGGGACAGTTGCAGT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3625	cg43945577	2581	CACTCTGCTGAACAGAATTTATTTT[C/T]TGAGTCAAATATAATTTATTATTAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3626	cg43945577	2696	CGTTTGCAAGAAGAGTTCCAGTTGA[C/T]GTGGTGTTTGGTTCCATGGCGGGGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3627	cg43945577	2744	GGTACCCTAGGGATTCATCTGTTTT[C/T]TTCACTTCCCTTTGCATCTGAGATC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16

3628	cg43945577	2784	CATCTGAGATCC TGCTGGAAACCA C[G/A]GCAACCT GTATCCACTATT AGGAGG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3629	cg43955093	1087	TCTCCTTTGTCA GGAATGCAAAAA A[A/gap]TCACAC ACTCCTACCAGG TGTTTTA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3630	cg43955093	1257	GCTCACGTTTGG GTACACATCATT T[T/gap]CTTGCA GTATTTCTAAAA GCTTTGC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3631	cg43955093	1277	CATTTTCTTGCA GTATTTCTAAAA G[C/gap]TTTGCC AGAGTCAAAAAT CCAAGTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3632	cg43955093	1288	AGTATTTCTAAAAT GCTTTGCCAGAG [T/C]CAAAAATCC AAGTTTGGATTC TAAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3633	cg43955093	1295	CTAAAAGCTTTG CCAGAGTCAAAA A[T/C]CCAAGTTT GGATTCTAAGCA GCCTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3634	cg43955093	1450	CTCATGTTACTA ACAGGCTGTAAC T[G/C]ATCAGCTG GATTAAGGAAAA AAGCT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16

3635	cg44014894	631	TTTCTACATCTG CAAGACAAGTTT G[G/gap]CTTCAG CCATTATGTATA GATAGAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC51331 CREB-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 2442 aa.	0	16
3636	cg43055918	353	ACATTCTCCCTT GAGGGAAAAAAA A[A/gap]GTGATT ATTTAAAATATGA GTAAAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
3637	cg43936393	383	AAACAAGTTTCA GTAAAAAAAAAA A[gap/A]CTAAAA CAAACACTGAAG TAGAGTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3638	cg43936393	398	AAAAAAAAAAC TAAAACAAACAC T[G/T]AAGTAGAG TTTTGTAAATACA ACTG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3639	cg43936393	719	CTTTAGGGAGGT GAGAACCTCCTT G[G/gap]CATATG CCCTACCTTAAT CTGAGCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3640	cg43947963	156	AGCACAGAGACT GGGGAGGGGTT GA[gap/C]CCCCA CTCCAGAACACC AATACCTC	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14667 KIAA0100 (HUMAN COUNTERPART OF MOUSE E1 GENE) - HOMO SAPIENS (HUMAN), 2092 aa.	0	17
3641	cg43947963	86	ATATCCTACGGG GAAGGGTAGGG GA[C/gap]CCATG GCCAGCCCTGG CTCCTACTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14667 KIAA0100 (HUMAN COUNTERPART OF MOUSE E1 GENE) - HOMO SAPIENS (HUMAN), 2092 aa.	0	17

3642	cg43949150	166	CTGTCTGGAGG GGCTGAGGCTTC GG[C/gap]CTCGG GAGGCTGAAGC AGGAGGCAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
3643	cg43949150	167	TGTCTGGAGGG GCTGAGGCTTCG GC[C/gap]TCGGG AGGCTGAAGCA GGAGGCAGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
3644	cg43964911	1457	TAGCTCACAGGT GAGGGGGTTTA GG[C/G]CCCCTC TAGGGAGCGCC TGAGGCCA	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa.	0	17
3645	cg43980727	406	CCTCACTCCAGC ACACTCAGCCAG G[T/G]GCCTGGC AAGATGACACAT TTCCTG	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0	17
3646	cg44023800	167	CCAGACAGACGA GGCCCGGGAAG GG[gap/C]AGCCC AGGGGACTGGG GTCTCTCCT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14521 GIANT LARVAE HOMOLOGUE - HOMO SAPIENS (HUMAN), 1015 aa.	0	17
3647	cg43957585	101	CCACAGACAGG CCTAGTATGGCT AC[G/A]GTACCGT ATATAAAAGACA ATTGCT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13433 ESTROGEN REGULATED LIV-1 PROTEIN - HOMO SAPIENS (HUMÁN), 752 aa.	0	18
3648	cg43979984	189	TTAACTTTGGAC AACTTAAAACTTA [T/C]TAGTGACAT TGCTGTCTAATA ATCA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92539 HYPOTHETICAL PROTEIN KIAA0249 - Homo sapiens (Human), 896 aa.	0	18

3649	cg44001797	1080	GCGCCTGCAGC ACGTTGCCTCCA GG[G/gap]CCCAG CCTCCCAGAAGC CTCAGAGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3650	cg44001797	185	TGTCTGTCAATT GCAATGCCTGG GG[C/gap]CAAGC CAGGCCAGTGG ACTTGTGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3651	cg44001797	324	ATGGGCTTGTGG AAGGGAGGCAT GC[C/gap]GCCGC CAGCATGCATGC CAGGGGTC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3652	cg44001797	719	AAAGTGAACGTA CTGAGACCGACA G[G/gap]ACAGCA AGAAGGCATTTG CACATTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3653	cg42555863	2867	GGAGAGGAGCC CCATGCCCAGCC TG[G/gap]CTGAG CCCGAGATTCGC TCCTCCCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14526 KIAA0290 - HOMO SAPIENS (HUMAN), 906 aa (fragment).	0	19
3654	cg42716880	95	GCAGTTTGGGG GTGGGGGACAA AGA[C/gap]CCCC CTCCAGCTCCTA AACTGGGTC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43360 F21856_2 - HOMO SAPIENS (HUMAN), 679 aa.	0	19
3655	cg43917942	2499	AGATAGCGAGAT CTAAATCTCTGC C[gap/A]AAAAAA AAAAAAAAACTT AAAAATT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19

3656	cg43917942	2500	AGATAGCGAGAT CTAAATCTCTGC C[A/gap]AAAAA AAAAAAAACTTA AAAATTA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3657	cg43917942	2514	AAATCTCTGCCA AAAAAAAAAAAA A[A/gap]CTTAAAA ATTAAAAACACA AAGAGC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3658	cg43917942	2831	CTCCCGCCCTG GCTCAGCTCCCG CG[G/gap]CCCCG CCCGTCCCCCCT CCCAGGAC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3659	cg43927434	97	TCTTTTTAAGGC AAAGCACCCGCA G[G/gap]TCAAGC CCCGCCCCGTC CCCCAGCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0	19
3660	cg43975166	3601	CCGCTGCTGCTG GGAAGACAGCA G[C/T]CTTGGCG CGTCCCACAATC CTGCGC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00267 SUPT5H PROTEIN - HOMO SAPIENS (HUMAN), 1087 aa.	0	19
3661	cg43982840	541	ATTACTGAAGGA AATAGAAAACTA T[C/A]TTACAAGT AGAACAGCCATA GACAA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O15063 HYPOTHETICAL PROTEIN KIAA0355 - Homo sapiens (Human), 1070 aa.	0	19
3662	cg44022290	177	AGAGGGGGCCT CCCCCTGAGGC CCC[gap/C]ATTG GCCCCCTCCCA GGTATCCAAG	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14145 KIAA0132 PROTEIN - HOMO SAPIENS (HUMAN), 624 aa.	0	19

3663	cg43919691	157	AACGTCTAGGGG TGAGGGGCTGT GG[C/gap]CTCCA GTCGGCCCCAC AGCCTTTGA	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3664	cg43919691	158	ACGTCTAGGGGT GAGGGGCTGTG GC[C/gap]TCCAG TCGGCCCCACA GCCTTTGAG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3665	cg43919691	349	ACTCGGCGGTG GCCCGGGGCTG CGC[C/gap]CAGG ATAGTGTTTATC AAATGTGAC	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3666	cg43919691	350	CTCGGCGGTGG CCCGGGGCTGC GCC[C/gap]AGGA TAGTGTTTATCA AATGTGACA	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3667	cg43919691	456	TTGTCTCTCATG GCTTCTCTCGGA G[gap/C]TACCGG AAGTTGGGCCTG GATAACG	gap	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3668	cg43919691	66	TTTTTTTTTTTTT TTTTTTTTTTTTT[A /T]CCGGGCACCA ACGTTGGTTTTA ATG	A	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3669	cg43921004	591	AGATGTCACAAA TTATAGCGGCAC C[C/T]GTTCAGAT TTAGGGTGAGTT TCTGA	C	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60506 GRY-RBP - HOMO SAPIENS (HUMAN), 623 aa.	0	20

3670	cg43921598	2636	AAAGCACCCGTA GTAGCAAAAACA T[A/gap]AAACAAA TAAAACTTCCCC CACATC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43439 MTG8-LIKE PROTEIN (MTG8 RELATED PROTEIN) (EHT) - HOMO SAPIENS (HUMAN), 604 aa.	0	20
3671	cg43958732	4278	TCTAAATAAATTG CTGTATTGTGCT[T/A]AATGTAAAAA AAAAAAAAAAAA AAA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3672	cg43958732	4281	AAATAAATTGCT GTATTGTGCTTA A[T/A]GTAAAAAA AAAAAAAAAAAA AAAAA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3673	cg43958732	4283	ATAAATTGCTGT ATTGTGCTTAAT G[T/A]AAAAAAAA AAAAAAAAAAAA AAAAA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3674	cg43317567	2185	TTCATCTCACTT CCAAATTTGGTT C[G/C]AAAGCAC AGTACCTAAAAA AGTTCA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60318 MCM3 IMPORT FACTOR (KIAA0572 PROTEIN) - HOMO SAPIENS (HUMAN), 1872 aa (fragment).	0	21
3675	cg44019279	4170	ATGCTTAATACG TGTCGGTCATAT A[C/T]AGTATTGA ATTTTTACTGTAT AGTA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14149 HYPOTHETICAL PROTEIN KIAA0136 - Homo sapiens (Human), 950 aa (fragment).	0	21
3676	cg43936123	163	ACGCTAGCACAG GGCCTGCCGCA GG[G/gap]CCTGG ATGCGGGCAAC GCAGGCGCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60289 KIAA0542 PROTEIN - HOMO SAPIENS (HUMAN), 968 aa.	0	22

3677	cg43936220	185	AGTCTCACTCAG AATATTTAATTGG [C/T]TTAAAATGA GAAAATGAATCT TTTT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75132 KIAA0637 PROTEIN - HOMO SAPIENS (HUMAN), 1171 aa.	0	22
3678	cg43959772	3077	AGGGGTGCGTA GGTAATGGCGTC GG[G/T]ACCGCT CGGTCGCTGTG GAGGGGTA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3679	cg43959772	561	AATATTTACTAGA ACAACATTTAAA[C/A]GTATCGTCG GTCCGCAGAAG CCTGG	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3680	cg43959772	882	AGGCAAGCCTCT AGATAGGCGGG GC[C/gap]AAGCC CTCCCCGTGCCC ACCCTCTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3681	cg43959772	886	AAGCCTCTAGAT AGGCGGGGCCA AG[C/gap]CCTCC CCGTGCCCACC CTCTTTCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3682	cg43955358	2322	AAACAACTTGA GCCTGTGCATAT A[A/gap]GGCATT TACATATGATGA CCTTGCA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4-GLUCANTRANSFERASE) AMYLO-1,6-GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)

3683	cg43955358	2360	TGATGACCTTGC ATCCTATAATAC A[A/gap]GTAATT GCATACTTAATA TCTGTAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4-GLUCANTRANSFERASE) AMYLO-1,6-GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
3684	cg43955358	77	CACAGAGGTAAC AATGACATTTGC C[C/T]ACTAGACA CAGTAGTTCAAG ACATA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4-GLUCANTRANSFERASE) AMYLO-1,6-GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
3685	cg43925474	1066	CACAGATCAATA CCACCTTGACTT G[T/G]TGACCCA GAGAATTCTAAT TAGATT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3686	cg43925474	1303	TCTCTCCCAATT AAAAAAACAAGA G[T/gap]TTTTTTG CTAGCTTGACAA TTTTAT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)

3687	cg43925474	2277	CGGCTTTTATAA GAAAAAAAAAAA A[A/gap]GACGAA TCTGTAATGAAG AAAAAAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3688	cg43925474	489	CATACTTTAATAT TATGTTGGTCCA[C/T]GGGGTATAC ACATTTTAACAAA AGA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3689	cg43925474	971	ATGGAAAGAAAA CAAAACAAGCAT C[T/A]TTTCAAGA AGAAATGAATTG GATAT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3690	cg43973809	2511	CCCCACCCCCA GCCTGGGGGTC TGG[T/G]CTGGG GCAGGGATTGCT CAGTGGAA	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p36.1)
3691	cg43973809	2559	GAAGCAGGACT GGGGGTCTGGC GTG[T/C]CCCCTC CCTGGGCCTCCA TCACCCC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p36.1)
3692	cg43973809	3160	CCGAGAGTCCA GGCCTTGCCTCC CC[C/gap]GACCG CCATGGAGGGG GCAGCCCGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p36.1)

3693	cg41573476	3166	AGAATAATACTA TTATAAGTTAGG T[gap/T]GACAAAT GATGTTGATTAT GTAAGG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3694	cg41573476	610	CCCTCCTACTCA GGATAAGACTTT C[G/T]AATTCTCC GGAGCTGAAAAA GGATC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3695	cg41573476	611	CCTCCTACTCAG GATAAGACTTTC G[A/C]ATTCTCCG GAGCTGAAAAAG GATCC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3696	cg41573476	612	CTCCTACTCAGG ATAAGACTTTCG A[A/T]TTCTCCGG AGCTGAAAAAGG ATCCT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)

3697	cg41573476	613	TCCTACTCAGGATAAGACTTTCGAA[T/A]TCTCCGGAGCTGAAAAAGGATCCTG	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3698	cg43117949	37	TCTGTCCACCAGCTGAGAAGGACAA[gap/A]GGGCGGAAGGCAGCTGCACAGAGCA	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10745 INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN PRECURSOR (IRBP) (INTERSTITIAL RETINOL-BINDING PROTEIN) - Homo sapiens (Human), 1247 aa.	0	10 (10q11.2)
3699	cg43117949	4091	TATATATGTATATATATATGGCTTT[C/T]CAATAACCACCTAAATTTTAACAAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10745 INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN PRECURSOR (IRBP) (INTERSTITIAL RETINOL-BINDING PROTEIN) - Homo sapiens (Human), 1247 aa.	0	10 (10q11.2)
3700	cg43920702	134	GGCTCTTGTCACCCACTCCTAACCC[gap/C]TCTGCAGATTTCCTCCGGGATGCTC	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3701	cg43920702	338	GAAACTAGGATTTCCAAATTCTGGA[gap/A]GCAGGACTGAAGTTATTTGGGGCAG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3702	cg43920702	36	TTTTTTTTTTTTTTTTTTTTTTT[A/T]TTTTTTTTAACAAAATGTATTCATC	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)

3703	cg43920702	439	AGGGGCTGAGT GGTCCTAGGCTC CC[gap/C]GGGCT GGAGGTGGGAC CTGTGCTCC	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3704	cg43920702	464	GGGCTGGAGGT GGGACCTGTGCT CC[gap/C]TTGGG TTAAGGGTGAAA CCTCAGCT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3705	cg43920702	812	TGGGCTCAGAGT TGGGGGACTAA GG[G/gap]CGGAG CCTGGGTCCCCA CAAGCGGT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3706	cg43269831	365	AAGAACTGTGGC CCCAGGATAAAA A[A/G]AATACAGT GAGAACAAAGAC CTCAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P15586 N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE) - *Homo sapiens* (Human), 552 aa.	0	12 (12q14)
3707	cg43950650	382	AGTAAAAGGGCG TTCCAAGTCTTG A[gap/T]TTTTTTTT TTTTTTTTTTTT AGCAG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99700 ATAXIN-2 - HOMO SAPIENS (HUMAN), 1312 aa.	0	12 (12q24)
3708	cg43950650	402	CTTGATTTTTTTT TTTTTTTTTTTT[g ap/T]AGCAGTAAT AGCAGCAAGAAT CACT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99700 ATAXIN-2 - HOMO SAPIENS (HUMAN), 1312 aa.	0	12 (12q24)

3709	cg43979900	1019	TCCTTCTTCCAG CCACCTGGAAAA A[C/T]GTTCACAG AGAGTTATAGTG GTTAC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3710	cg43979900	1116	AATTAATCTGCT AATATCTATTACC [G/A]CAGAAATAG TGTTAGAGGTAG TTTA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3711	cg43979900	1147	ATAGTGTTAGAG GTAGTTTATTAAA [G/C]AGGCGTTTT TAAAATCATCCC ACTC	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)

3712	cg43979900	1152	GTTAGAGGTAGT TTATTAAAGAGG C[G/A]TTTTTTAAA ATCATCCCACTC ATCAT	G	A		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3713	cg43979900	157	AACCACTGAATC ACACAACATGGA C[C/A]AATCTCAA ATCATTATGCTG ATGGA	C	A		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3714	cg43979900	292	ATTCCTATCAAT GGCTGCCAACAA T[T/C]GGGAGTG AAAGGAACTGAC TGAGCA	T	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)

3715	cg43979900	470	AAATAAATTACA CCTCTATAATGT T[T/C]GTTTTAAA AAATATTAGATA CATCA	T				SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3716	cg43979900	616	TAGCTAAGCCTA TGTTAGACTCTT A[C/T]AAATTCCT AAATAGTAGAAT TAGTT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3717	cg43973740	669	AGGTCCTGAAGG TGAGTGTCCGGA G[G/gap]TGCTGG GTAAAACACATC ACAGGTA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0	16 (12q12)
3718	cg44928323	10345	TAAAATTGGTTTT GATACTCAGAAA[A/T]AACAAGAATT TAATTTTTTAAAT TT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
3719	cg44928323	11285	GACTTGTTAAAG AGGAAACCAGGA A[C/T]TCAGTCAT GTTTTTGTCCTG GATAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)

3720	cg44928323	11963	ATGATAACTTAC TGTCCTTTCCAT C[C/T]GGGCCTA AACTTTGGCAGT TCCTTT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
3721	cg44026807	2058	GGAGGAAGAAG CCCCGTTTCCAG G[C/gap]ATCCG CAGCCCAGGGT AGGGAGAAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14397 GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR) - Homo sapiens (Human), 625 aa.	0	2 (2p23.3)
3722	cg43960198	2178	CGGCCGGGCCC GGGGCTGAGGT CAG[C/gap]CTCA CTGCCTGCTTAT TGCCTCTTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3723	cg43960198	2474	TGCAAGGCTGG CAGCCCCCACC CCC[gap/C]ACCC CCCAGGCCGCC TTGAGAAGCA	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3724	cg43960198	2491	CCCACCCCCACC CCCCAGGCCGC CT[T/gap]GAGAA GCACAGTTTAAC TCACTGCG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3725	cg43960198	2505	CCAGGCCGCCTT GAGAAGCACAGT T[T/gap]AACTCAC TGCGGGCTCCT GAGCCTG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)

3726	cg43960198	2700	GGCCCCATGCCT CTCCTCCCTCTC T[gap/C]GGCAGG GCCCCATCCTGG GCAGAGG	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3727	cg43960198	2708	TGCCTCTCCTCC CTCTCTGGCAGG G[C/gap]CCCATC CTGGGCAGAGG GGCCTGGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3728	cg43960198	2711	CTCTCCTCCCTC TCTGGCAGGGC CC[C/gap]ATCCT GGGCAGAGGGG CCTGGGGCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3729	cg43960198	2734	CCCATCCTGGGC AGAGGGGCCTG GG[G/gap]CTGGG CCCAGAGTCCAG CCGTCCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3730	cg43956384	2427	GTACCTACTGGA GCCGCAGAAGG GA[A/gap]GTCCA CTCAGTCACATC CAGAAAAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P13866 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)
3731	cg44025634	3380	TTTGTGGGGGAA AACTATTAATTTT [T/G]TGCAAATGG AAAGATCAACAG ACTA	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)

3732	cg44025634	3873	TGGCAGATGTCA CATGAGTAGAAT T[C/T]CTGCCCAG CCTTAACTGCAT TCAGA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
3733	cg44025634	3985	GACACATGGTTG TGAATACAATGA T[G/A]TATTTCTT TATTTTCACATAC ACTC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
3734	cg44025634	4039	TAAAAGAGCAAG AGTACACATCAA C[gap/A]AAAAAT GGAAACAAGGCT TTGGCTG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
3735	cg43955813	3033	TATATGTATGTAT ATATGTATATGT[G/gap]AAAACAG TTTGTATAGTTG GAATA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0	4 (4q12)
3736	cg43993542	322	CGGTTTTCTGGG CTGGGCTTTCTG C[C/gap]TTACTC ACTCCTTCTCCC TCTTTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16471 PROLACTIN RECEPTOR PRECURSOR (PRL-R) - Homo sapiens (Human), 622 aa.	0	5 (5p13)
3737	cg43993542	449	CTGATGTGGCAG ACTTTGCTCCCT G[G/A]CAAAACTA AAGAACTCTCCT ATTCA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16471 PROLACTIN RECEPTOR PRECURSOR (PRL-R) - Homo sapiens (Human), 622 aa.	0	5 (5p13)
3738	cg43952287	161	TGTAAAAAGCA AACAGTGCCAAT G[G/gap]CCACTT TGGTAAAAACAC ACAGTGT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0	5 (5pter)

3739	cg43952287	92	TTTTTTTTTTTTT[C/T]CTGGTTGACAAATTTTCTTTACTTA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0	5 (5pter)
3740	cg43952287	93	TTTTTTTTTTTTT[C/T]TGGTTGACAAATTTTCTTTACTTAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0	5 (5pter)
3741	cg43955232	7346	GAGAGAATTACACTTTTTTTTTTTT[gap/T]AAGTGGCGTGGAGGCCTTTGCTTCC	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54253 ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN) - Homo sapiens (Human), 816 aa.	0	6 (6p23)
3742	cg42907760	2137	CTGCCCTGCTCTGTGACAGAGCCTG[gap/G]AGACTTGGAGGTCCAGAGGCCCCCC	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3743	cg42907760	2149	GTGACAGAGCCTGAGACTTGGAG GT[gap/G]CCAGAGGCCCCCCACCAACCAGCCC	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3744	cg42907760	2174	CCAGAGGCCCCCCACCAACCAGCCC[gap/C]AGCCACTGTTGCTGGCTGTGTCGTT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3745	cg42907760	2174	CCAGAGGCCCCCCACCAACCAGCCC[gap/C]AGCCACTGTTGCTGGCTGTGTCGTT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)

3746	cg42907760	2272	CTGTTGCCACTT ACGGGGGCTGG AG[A/gap]AGGCC TGGATAAAGACA GAAGGGCG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3747	cg42907760	2273	TGTTGCCACTTA CGGGGGCTGGA GA[A/gap]GGCCT GGATAAAGACAG AAGGGCGG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3748	cg43958842	632	CCATTTGAATTT CAATCCAAGCAG C[A/G]TATTTTAC ACACACCTGAAG GAAAT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P41252 ISOLEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (IRS) - Homo sapiens (Human), 1266 aa.	0	9 (9q21)
3749	cg42373006	59	TACACAAATGAA GTCTTTGGTGGA T[G/A]AATTCAAG TCAAAACAAATA ATAGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60267 KIAA0512 PROTEIN - HOMO SAPIENS (HUMAN), 632 aa.	0	X
3750	cg43921793	1986	GGATCTGCAGCA GCTGGGCTGCC TC[C/gap]GATGG TGGAGAGCTGG ATGAAGGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
3751	cg43921793	42	CGACTTTTTTTTT TTTTTTTTTTTT[T/ G]CAGACTTTTCA GCTTTTATTACAA A	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X

3752	cg43921948	3315	AACAATGTGATT GGATTCCTTTAT G[G/C]CAAAATC GAGAGAAGCTG CCATCCA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3753	cg43921948	3494	GAATGTTAGCCA TGACTTGGGCTT T[C/G]TGAAAGTT GGCTATAATTTC TCTAT	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3754	cg43921948	3989	TTGATGATGTGG AAATGCTGCAGG A[T/C]TAAATAAC TTGAAGAGCCTT TATAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3755	cg43921948	4592	TATGGTACTAAG GAAGTCCTGTTT T[T/gap]CAAAAAT GGAAGCCCACTT CTCAGA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3756	cg43921948	4665	AAAAGTGAAGGG GAAACACACACA C[A/G]CAAAAAAA CAAGTATTTGGC TTGTC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X

3757	cg43921948	4673	GGGGAAACACA CACACACAAAAA AA[gap/A]CAAGT ATTTGGCTTGTC ACAGGAAT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3758	cg43921948	4717	CAGGAATCTGAT TGCATTAAGTGA A[A/gap]GGATTA TTTAGAATATGTT AATGCA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3759	cg43921948	5894	CAGGTGATGTCT GGTCAACTGGCC T[A/G]CCTTCAGC TAGAATCCTGTT AGGTC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3760	cg43921948	5975	CTTGGTAATCTT CCATCCACTGCC C[C/A]TGACCCTG TTCCCTGTCTAT AAATC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3761	cg43921948	6017	CTATAAATCCCC AGTTTTCCATGG T[G/A]TATTCAGA GCTGAGTCCAGT CTCTC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X

3762	cg42866508	1928	TTCTCCAGTCAG AGTAGATGATGA G[G/gap]CCCATG CCCCTCACCCCC ACGCCCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76007 TRIPLE LIM DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 615 aa.	0	X (Xp11.23)
3763	cg43927750	276	ACTGTATTTGAG ATGTCTTACTTG G[T/G]AGACCAAT TAAACTATGACA TAAAA	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
3764	cg43927750	631	ATTGAAATGCAT AAACACAATACT T[T/gap]CAAGAAT ACGCTCAACACA TGTACA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
3765	cg43277466	593	TCGCCAAGCAGA CACAGAAATCCC C[A/G]TGTGGGG GAATGCAGCAGC TCTGCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	XY
3766	cg43061097	4045	TGATGCATGTTG GCTGAGATGATC A[T/G]GGAGATG AGTGACACCAGA GCTCAC	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD39482 OLIGOPHRENIN-1 LIKE PROTEIN - HOMO SAPIENS (HUMAN), 814 aa.	0	
3767	cg43061097	4046	GATGCATGTTGG CTGAGATGATCA T[G/T]GAGATGAG TGACACCAGAGC TCACA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD39482 OLIGOPHRENIN-1 LIKE PROTEIN - HOMO SAPIENS (HUMAN), 814 aa.	0	
3768	cg43273039	4922	ATAAATTAAATTT TATTGTGTAAAA[A/T]AAATTATTAC ATAAAATGTGTTT TT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75763 SYNAPTONEMAL COMPLEX LATERAL ELEMENT PROTEIN - HOMO SAPIENS (HUMAN), 1530 aa.	0	

3769	cg43273039	4924	AAATTAAATTTTTA TTGTGTAAAAAA[A/T]ATTATTACAT AAAATGTGTTTTT GA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75763 SYNAPTONEMAL COMPLEX LATERAL ELEMENT PROTEIN - HOMO SAPIENS (HUMAN), 1530 aa.	0	
3770	cg43277456	2654	GACCGACAGTC GTGAGGATGGC AGA[G/gap]CTGC TGCATTCCCCCA CATGGGGAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	
3771	cg43277456	2673	GGCAGAGCTGC TGCATTCCCCCA CA[T/C]GGGGATT TCTGTGTCTGCT TGGCGA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	
3772	cg43291710	555	GACAGTCTGAAG CATTAAAAAATTC [G/A]TAAAAAACA GTAACACTGACA AAAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA34522 KIAA0802 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	0	
3773	cg43916588	1102	GGTCCATGGTGT TCCAGAGTCCCC T[G/A]AGTTTCAG GTTCAGCTGATG TAGAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	0	
3774	cg43916588	352	GCCACCAGGAT GAAAGCAGGGTT AG[G/gap]TCCAG GGACCCAGTAGA GCCTTGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	0	
3775	cg43918446	1527	CTAAAAACTGAT TTGCAAACTTGA A[C/A]GTCTAGAT GTGTGTAGGAAG ATTTT	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	

3776	cg43918446	1559	ATGTGTGTAGGA AGATTTTAAAATT [T/C]AGGCAAATT GGTCTCTAAAGA GACC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3777	cg43918446	1570	AAGATTTTAAAAT TTAGGCAAATTG[G/gap]TCTCTAAA GAGACCAATTTT GCTTC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3778	cg43918446	1926	TGTTTTTCCCCA GGAACTATTGAT G[A/C]CTGAGGA GACTTGAAAAGA GACCTA	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3779	cg43918446	1930	TTTCCCCAGGAA CTATTGATGACT G[A/G]GGAGACT TGAAAAGAGACC TAAAGT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3780	cg43918446	2125	TCTCCATGTGGA GTAGGTCAAAGT C[T/C]CCGTCCTC CCTGGCCAGGT GGAAGC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3781	cg43918446	444	CAAAAAATAACA ATCCAACAAGAG T[C/A]ATGTTACC CATTCTTAGCCA TTAAC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3782	cg43918446	529	TGTACCCAACTG GGACCAAATACA A[A/gap]CATGAG ACACTAGGGTGG CTTGTCC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	

3783	cg43918446	601	AAGGAACTTTAT CATGGGCTGAGA G[T/A]TAGATAGA TAGCTTAGAACA ACATT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3784	cg43918446	655	AAAGTGGGTGCT TCTACATGAGGA C[T/gap]TTTTTTC CCCCCAAGTAGA AAAATA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3785	cg43918446	661	GGTGCTTCTACA TGAGGACTTTTT T[T/gap]CCCCCC AAGTAGAAAAAT AATTAAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	
3786	cg43920875	2433	GTTCTGACTCCC AGTACGGTGTTG T[G/T]GCGCCGC TAGGATATCCTT GTCAAG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR (IF-2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0	
3787	cg43920875	2434	TTCTGACTCCCA GTACGGTGTTGT G[G/T]CGCCGCT AGGATATCCTTG TCAAGG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR (IF-2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0	
3788	cg43923595	310	CCGGCAGTCCCT GCCCAGTCCCTC C[G/C]TCTGCTTC CTCCCACTCTTC CACAT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99467 LYMPHOCYTE ANTIGEN 64 PRECURSOR (RP105) - HOMO SAPIENS (HUMAN), 661 aa.	0	
3789	cg43932090	19	TTTTTTTTTTTT TTTTT[G/T]AAGG TTCTCAAGAATTT TATTATAA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	

3790	cg43934688	2862	GTCTTCATATGT CAACTACAGAAA A[A/G]AAAAAAA ATAGAAATTGAA GGATT	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3791	cg43934688	2863	TCTTCATATGTC AACTACAGAAAA A[A/G]AAAAAAA TAGAAATTGAAG GATTT	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3792	cg43934688	4242	ACTTTTTATGTCA TCGTAAAAGCTG[A/gap]AAAAATC CCTTTGTTTCTAT TTAT	A	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3793	cg43934688	4248	TATGTCATCGTA AAAGCTGAAAAA A[A/gap]TCCCTTT GTTTCTATTTATA AAAAA	A	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3794	cg43935504	70	ATTTTAGCACAG TTAAATTTTTTTT[T/G]TGTAAACAC AAACAAGATAAA TTTA	T	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15044 KIAA0335 - HOMO SAPIENS (HUMAN), 1263 aa.	0	
3795	cg43936083	239	AAGTCAACAGGG AAAGAAGTGGGT A[C/gap]CCCCTT TGCCAGAAGCTA ATTGTTT	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3796	cg43936083	323	AAGATGTAGGCA GTGGCGGCAGG CC[C/gap]TGCGC CCACAGCTCCTC GCCTGTCC	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	

3797	cg43936083	335	GTGGCGGCAGG CCCTGCGCCCA CAG[C/gap]TCCT CGCCTGTCCTTT GACCACAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3798	cg43936083	432	ATGATAGGGGAA CAATAGAGGGGA A[C/gap]CCAGCC TCAACCCAAGTC AGAAGGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3799	cg43940146	185	AAACTCATTACT ATAAATTATTCTT [A/C]CAGTACTTT GCAAATTCAGAA TTTC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15910 ENHANCER OF ZESTE HOMOLOG 2 (ENX-1) - Homo sapiens (Human), 746 aa.	0	
3800	cg43940465	662	CCTTTGGGTCAG TGTGTTAATTAG G[G/gap]CTGAGA GCCTGGGTGAAA GGCAAGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0	
3801	cg43951590	167	CTGATAAAACAC ATACAAAAGTTA A[A/G]AGACAGCT CGATTTCATCTT CCTCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14684 HYPOTHETICAL PROTEIN KIAA0179 - Homo sapiens (Human), 740 aa.	0	
3802	cg43951590	2663	TACAAAATCATA AAAAAGCCCCCA T[T/A]TTCTTAAA GGTATAATTTATA GCGC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14684 HYPOTHETICAL PROTEIN KIAA0179 - Homo sapiens (Human), 740 aa.	0	
3803	cg43960583	6448	CTGCTGTTTGCT TAAAAAAAAAAA A[A/gap]CACCCT TGTCATGTATTTT CTGTAT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q93073 HYPOTHETICAL PROTEIN KIAA0256 - Homo sapiens (Human), 635 aa.	0	

3804	cg43971555	235	TGAGCTTCAGGC GGTTGTCCCGAA G[G/gap]GTCAAG TGGCCAGCAGG GTCTGGTC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0
3805	cg43971555	236	GAGCTTCAGGC GGTTGTCCCGAA GG[G/gap]TCAAG TGGCCAGCAGG GTCTGGTCG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0
3806	cg43975476	95	TATTATTTTCCTT TGGAAGAAGAAA [C/A]CAGAAAAAA AACTTCCTGATT GTAA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75141 KIAA0650 PROTEIN - HOMO SAPIENS (HUMAN), 848 aa (fragment).	0
3807	cg43979857	123	ACGCAAGACAGA TGATGCAGGGG AA[C/T]GGGTGTC CACTCTTTCTTG TTCTCA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60327 KIAA0584 PROTEIN - HOMO SAPIENS (HUMAN), 738 aa (fragment).	0
3808	cg43981392	25	TTTTTTTTTTTTT TTTTTCTGCAA[T/C]TTGAGGAACA GTTCACTGATTT ATT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15297 WIP1 - HOMO SAPIENS (HUMAN), 605 aa.	0
3809	cg43985672	614	AGTGGCTGGGA CAAGCTGGCGG GGG[C/gap]CAAG CACTGTTGAAGC AATAGGGTC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15017 ORF - HOMO SAPIENS (HUMAN), 692 aa (fragment).	0
3810	cg44001705	274	TGTTTTCCATAC AAGACTGTCACG C[A/G]AAGGATCA ATTTGTGCATGT GCCAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00539 NUCLEAR PROTEIN SA-1 - HOMO SAPIENS (HUMAN), 1258 aa.	0

3811	cg44003843	6105	CAGAAATGTAAG TCAACTTAAGAA C[A/G]GTGAATGA ATGTAAAAACAT TCAGT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0
3812	cg44003843	6131	GTGAATGAATGT AAAAACATTCAG T[C/T]GAGACCAT ATGCATTTTCTG TGCTG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0
3813	cg44009187	1459	ATGTCCGTCACG CGGCTAACTTGA C[C/gap]TGGCGG GTCTAAGGAAAG TCAACTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0
3814	cg44009187	18	TTTTTTTTTTTTT TTTT[G/T]ATGGT TTCCATTTTTTTC CTTTAAT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0
3815	cg44022781	275	ATCTCTTGAGCT CTTTCCCACTGA C[T/G]TGTCATTC ACAGGCATTCAA ACTGT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa.	0
3816	cg44036048	65	TTTATTTCAGTTT TGGCTCTTAAGC[C/gap]ACTTCCAT TGGGAAGAAGAA ACTCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45768 HYPOTHETICAL 94.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 851 aa (fragment).	0
3817	cg44130923	5459	ATGTCCATAAAG TGGCGTGAAGTG A[A/G]ACGTTCTC TTTGGTGGTCAA CCCGG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) - MUS MUSCULUS (MOUSE), 1726 aa.	0

3818	cg44921672	1595	GCAAAAAATTAG CCAGGCATGGT GG[C/T]ATGCAC CTGTAGACCCAG CTACTTG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O60879 DIAPHANOUS PROTEIN HOMOLOG 2 - Homo sapiens (Human), 1101 aa.	0	
3819	cg44921672	1648	AGGCTGATGCAG GAGGATCGCTTG A[A/G]CCTGGGA GTTTGAGGTTGC AGTGAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O60879 DIAPHANOUS PROTEIN HOMOLOG 2 - Homo sapiens (Human), 1101 aa.	0	
3820	cg44932392	194	AATTTTATGTCCT TTAAGATACATT[A/gap]AAAAAAA AAAAAAGACACA TCAAC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
3821	cg44932392	208	TAAGATACATTA AAAAAAAAAAA A[A/gap]GACACA TCAACTGCAAAC GTGAAGG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
3822	cg43942696	1416	TTCTGGGCCCTG TCTGCGGTTCCA C[A/G]TGTGATAC TGTGGGTGAGAC GGCAT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3823	cg43942696	1438	CACATGTGATAC TGTGGGTGAGAC G[G/C]CATGGCC CATTCCTGCACT TGGCCA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8

3824	cg43942696	172	TCAAGACAGTGG TTACAAAAAAAA A[A/gap]GTACTC TTCTGGCTACAC ACTTTAT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3825	cg43942696	260	CAATCACAATTT CCAGGATTAAAA A[C/T]CATCTATT CTTAAATCCTAC ACTGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3826	cg43942696	274	AGGATTAAAAAC CATCTATTCTTAA [A/G]TCCTACACT GTTTTAGAGCAT CAAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3827	cg43942696	480	CAAAACAACCAA AAATTACCATGA C[C/T]CGGTACA GGAAAAACAGGA AGACTC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3828	cg43942696	69	AACAACCACATT TTGCTTTATTAG G[C/T]GTTCCATG GTAATATAACAC AGAGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8

3829	cg43957199	387	CAGATGGGTGG GGCAGGGTGGG GTT[C/gap]CCCC CATCTGACCCTC TAGGGCTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
3830	cg43957199	392	GGGTGGGGCAG GGTGGGGTTCC CCC[C/gap]ATCT GACCCTCTAGGG CTCTGGGGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
3831	cg44002959	3908	CCTTGTGGGGG GACCAGGGCAG GGC[C/gap]TGGG ACAGGGAAGGG GGTGAGTTAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92513 MYELOBLAST KIAA0239 - HOMO SAPIENS (HUMAN), 571 aa (fragment).	1.4e-316	5
3832	cg43958391	253	CCCCCGGGAAC AGAAGGCAGTGA TG[C/gap]CAAAT GCCAAGGAAGC AGCTTAAAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14545 FLN29 - HOMO SAPIENS (HUMAN), 582 aa.	2.4e-316	12
3833	cg43958391	254	CCCCGGGAACA GAAGGCAGTGAT GC[C/gap]AAATG CCAAGGAAGCA GCTTAAAAC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14545 FLN29 - HOMO SAPIENS (HUMAN), 582 aa.	2.4e-316	12
3834	cg43937128	170	CACAACTTGATG GTTTTTTTTCTTT[C/T]TTTGCAAAA GGACAATCTATA TGCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2-2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X

3835	cg43937128	299	GGCTGGAGGAG GTATACAGGATA AC[A/gap]AAAAA AAAAAAATAGAA AAAAATAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2-2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3836	cg43937128	311	TATACAGGATAA CAAAAAAAAAA A[A/gap]TAGAAA AAAATAAGAAAG TGGTTCC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2-2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3837	cg43937128	311	ATACAGGATAAC AAAAAAAAAAA A[gap/A]TAGAAA AAAATAAGAAAG TGGTTCC	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2-2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3838	cg43979183	1210	CCATGCCTGACA AGTTCTGAAGAG G[A/gap]AAAAA AAAATTGTTTTAA TCCAGT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3839	cg43979183	1219	ACAAGTTCTGAA GAGGAAAAAAAA A[A/gap]ATTGTTT TAATCCAGTTTC TGTCTG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3840	cg43979183	1220	CAAGTTCTGAAG AGGAAAAAAAA A[A/gap]TTGTTTT AATCCAGTTTCT GTCTGC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3841	cg43979183	1300	CCCTTTATGAAA AGATAAAGCAGA A[C/G]AAAAGTGA AATATATCTTCA GATTA	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	

3842	cg43979183	754	TCTCAATATACA CACAGATTAAGA G[T/gap]TTTTTGC CTTGGCAAAAAT AAAACT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3843	cg43979183	759	TATACACACAGA TTAAGAGTTTTTT [gap/T]GCCTTGG CAAAAATAAAAC TGAAGT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3844	cg43979183	872	AAAGATTACAAT ACATTATTAACTT [A/C]CTTTTTAAA CACAGAGTAAAG TTAC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3845	cg43979183	873	AAGATTACAATA CATTATTAACTTA [C/A]TTTTTAAAC ACAGAGTAAAGT TACT	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3846	cg44002835	22	GTCGACTTTTTTT TTTTTTTT[A/T]TA TAAAAAGGTCAC TTTATTTTGCC	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13585 MELATONIN-RELATED RECEPTOR (H9) - Homo sapiens (Human), 613 aa.	5.0e-312	12
3847	cg44002835	406	GAGTCTGACAGT GTTCGGGCTGCT G[C/gap]CTTTATA GTCTGTGTTCTC AAAGTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13585 MELATONIN-RELATED RECEPTOR (H9) - Homo sapiens (Human), 613 aa.	5.0e-312	12
3848	cg43948793	394	GCCACACAAATC TGTGTGTGGCTA A[G/C]GATGAGG ATACAGAGAAAA GAAAAA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15051 HYPOTHETICAL PROTEIN KIAA0036 - Homo sapiens (Human), 598 aa.	5.5e-315	6

3849	cg42710561	1866	TGAGGAAATGTATAAAATACCACAT[A/G]GTATAAAATTACATGTTAATACAAT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92521 PIG-B - HOMO SAPIENS (HUMAN), 554 aa.	6.1e-311	15
3850	cg43938133	1324	CACTTCGGAAGTCCCAAGGGCAGTG[C/gap]GGATGACCGATTTGGCCATGGAAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14195 DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (UNC-33-LIKE PHOSPHOPROTEIN) (ULIP PROTEIN) - Homo sapiens (Human), 570 aa.	6.6e-310	5
3851	cg43938133	1846	ACTTATTCAAACCTGCAGTCAGAGA[C/T]AATGGTTTCTCCTAAGCAATTAAAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14195 DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (UNC-33-LIKE PHOSPHOPROTEIN) (ULIP PROTEIN) - Homo sapiens (Human), 570 aa.	6.6e-310	5
3852	cg43277973	62	TTTTTCTTTTCACAGTCCGCCTCTT[gap/C]TAATCTTGGACTGGAGGATATACAG	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P36269 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYLTRANSFERASE 5) (GGT-REL) - Homo sapiens (Human), 586 aa.	8.0e-314	22
3853	cg44015618	348	GGCAGGTTGATCTGGGAACGGGCTG[G/A]CATGCTAGGGATGGTGGAGAAGTAG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
3854	cg44928804	2623	AATGAGAAAGGCCAGAGGCTGCAAA[A/gap]GACAGTCAAAGGACACGAGAGAAAG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)

3855	cg44928804	3388	CCTCGGTTCTAT GCATATATGGAT T[A/gap]GCTATAA AAAATGTCAATA AGATTG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3856	cg44928804	3435	ATTGTACAAGGA AAATTAGAGAAA G[G/T]CACATTTA GGGTTTATTTTTT ACAC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3857	cg44928804	3493	TAAAATAGGGTA AATCCTATTAGA A[gap/A]TTTTTTA AAGAACTTTTTTT AAGTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3858	cg43956210	1844	ATCATGTAAAAT AAGATATTAGAC T[G/gap]TTTTTTG AATAAAATATTTT TATTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA- GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
3859	cg43982721	1884	CTCTCCTAGACG CCCAGGACCGG CC[G/gap]CCCTG TGAGCCGTGCTG GCCCCACC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	
3860	cg43982721	1937	AGGCCGCGGGG CCCCAGGGCAC TCG[C/gap]CCCC CTCCTTAGCATT TTCTTTTGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	

3861	cg43955051	136	AATTTATGGTAA CAATCATTTCTTT [T/C]AAATGTCTA ACTTATTTAACC CCTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD10823 SQUALENE EPOXIDASE (EC 1.14.99.7) - HOMO SAPIENS (HUMAN), 574 aa.	1.9E-305	8
3862	cg43264444	216	GGAAGAGGGAA AAAGGTTGCTTC TG[T/C]TTTATTTT CACATCTGTAAT TTTAA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene REMTREMBL-ACC:G513351 PROTEIN 1 - ARTIFICIAL SEQUENCE, 530 aa.	2.4E-305	11 (11q21)
3863	cg43991434	194	CATCTGCCCAGT CCAGACCCTACC G[C/T]TCCCCTGC CCCAGGAGGTC CTTTAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3864	cg43991434	427	ACAATCTGGTGT CTGCCTGTCCAC A[C/T]GGTGTGG GGCCCAGGGTT GCCCTCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3865	cg43991434	59	TTTTTTTTTTTT TTTTTTTTTTT[G /T]AAGCTGCCAC ACGACTTTATTT GTG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3866	cg43991434	828	TCCCCACAACAG AGCAGGGCTGG GC[C/gap]AGCAG AAGACGTTAAAA CCCAAATC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3867	cg43962078	2297	TCTTTCTGTCCTT TTAAGTGTACCT[G/T]GAATTCTTT GATTTATTTTATT GCA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O43776 ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE-- TRNA LIGASE) (ASNRS) - Homo sapiens (Human), 548 aa.	2.2E-304	18

3868	cg43962078	2507	ATAATCCTGAGG CATAGAAATTGA A[A/G]AATTTGTA AAAATAGAATTG CCTTA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O43776 ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE-- TRNA LIGASE) (ASNRS) - Homo sapiens (Human), 548 aa.	2.2E-304	18
3869	cg43985349	3532	TGCCATGGTGCG GGCCGGGGCGG AC[G/A]CGTTCCC ACCTTTGGGACC GGACGG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC69991 GLYPICAN-4 - HOMO SAPIENS (HUMAN), 556 aa.	2.7E-304	X
3870	cg43951838	334	CTTTCTGAGTGT GAACCTGGCTCG G[C/gap]CTGAAG CCTAGAGCTGGC TTGAAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3871	cg43951838	82	TTTTTTTTTTTTT TTTTTTTTTTT[G /T]TGGGCAGTTC ATTTTCTTTATTT TT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3872	cg43951838	84	TTTTTTTTTTTTT TTTTTTTTTTGT[G/T]GGCAGTTCA TTTTCTTTATTTT TTC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3873	cg43142595	591	CCTGGTGCTGCT GAGATGGGCGC TG[C/gap]CTCCT CCCACCCACAGC GCGTCATC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	

3874	cg43142595	592	CTGGTGCTGCTG AGATGGGCGCT GC[C/gap]TCCTC CCACCCACAGC GCGTCATCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3875	cg43142595	703	CCCGCACCCAG ACCGTGCCGTCT GG[C/gap]AGGCA CTTTCGGCCTCA GTGCCACG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3876	cg43142595	745	AGTGCCACGGC CCCCTCCCCAG GCC[A/G]CTCAC ACTCCTGGGGG GCCACAGAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3877	cg43142595	753	GGCCCCCTCCC CAGGCCACTCAC AC[T/C]CCTGGG GGGCCACAGAG GTGTCTGC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3878	cg43142595	910	GGGCGGGCCCT TGACACTGAGGC TG[gap/C]TCCCG CCCCCACAGCA GCCTGGCGA	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3879	cg43317253	3037	GGTCCTGTTTTC TAAAAAAAAAA A[A/gap]CTGTTG TAGAAATTCTTAA TTTGGA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2E-301	9

3880	cg43317253	3219	ATTAAAATCTTTC TTTGGGGAAAAA[A/T]TCTTGGTTAT TCTGCCATAACA GAT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2E-301	9
3881	cg43917155	2849	CATACTGTGTCT GTGAGTTTCTTC A[A/G]TTACAAAT GGGCATTTAGTA TAGTT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
3882	cg43917155	3090	GATCTCTTTGCT GAATTAATGAGT T[C/A]TTAACATG TGGACCCAACTG CCTGT	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
3883	cg43988371	4038	TTCTGTGACTAA TCACTGAACTAG A[C/T]GAATGTTA AATTTTTTATGTC TGAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA34487 KIAA0767 PROTEIN - HOMO SAPIENS (HUMAN), 573 aa (fragment).	4.1E-301	22
3884	cg44916647	322	ATGTCAACCTGC CCGACCCTCTGG G[G/gap]TGAACT GGATGTGGACAC TGGAGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
3885	cg44916647	496	TGTACATGTAAC ATGTGGCCATGC C[C/gap]AGGCAT CCCAGCATCTAT CCTGAAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
3886	cg44916647	507	CATGTGGCCATG CCCAGGCATCCC A[G/A]CATCTATC CTGAAGTCAGTG TAAAG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1

3887	cg43296397	575	GACACTGAGAG GTTTCCATCTGC AG[T/C]GCCAAG GGCTGCAGGTTC TGCCATG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14134 ATAXIA-TELANGIECTASIA GROUP D-ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 588 aa.	7E-299	11
3888	cg43923376	1791	TGAGCAGGAGTT TGAACAGACCTG A[G/gap]CCCCAG GCACCGAGGAG GGTGCTGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
3889	cg43923376	1867	GGCTTCCACTGC ATCCTGGCCAGG G[G/gap]ACGGAG CCCCTTGCCTTC GTGCCCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
3890	cg43280144	514	TCAGAATTTAAA GCCTCCCCACCT G[A/C]AAGATTAC ATATATAAAACTC CCAC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15320 MEA6 - HOMO SAPIENS (HUMAN), 804 aa.	7.4E-295	
3891	cg43255486	1897	CTCCACCCATCC AGTGGACTCTGG G[G/gap]CGCGGC CACAGGGGACG GGATGAGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.7E-294	17
3892	cg43998124	189	CCAACTCTGTGA ATTAGTATTAAG C[A/G]TAACTATC ACATATGTAAAC GCGAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	

3893	cg43998124	343	CTTGCAAACAAA GAATTACTAATTT [A/C]AAGTGTAAA AATTTTGCAAAG GGAA	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	
3894	cg43981656	1171	TGAATATTGTAA ATATTACAATTG G[gap/G]TATTAG AAAGCCATGATG AATCCAG	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3895	cg43981656	1269	ACCAGGCTTACC ATGTTCTAAATAA [C/T]TCAAGAAAA TATCTTTAAAAAA AAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3896	cg43981656	1294	TCAAGAAAATAT CTTTAAAAAAAAA [gap/A]GGACTGC AATTTAACAGTA ATCTGT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3897	cg43981656	1345	ATATCTTTAGCT GCCATTAAAAAA A[G/A]AAAAAAGA ACAACCAAAAAC AATGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3898	cg43981656	809	TCAGGAAGAAAA ATACTTTAAAGA C[A/G]TGCCAATT TGAAAAGGCATC AAAGT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3899	cg43981656	820	AATACTTTAAAG ACATGCCAATTT G[A/T]AAAGGCAT CAAAGTAAAAAA ATAAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10

3900	cg43981656	821	ATACTTTAAAGA CATGCCAATTTG A[A/T]AAGGCATC AAAGTAAAAAAA TAAAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3901	cg43981656	833	CATGCCAATTTG AAAAGGCATCAA A[G/A]TAAAAAAA TAAAAGCAAATG CTAAA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3902	cg43981656	841	TTGAAAAGGCAT CAAAGTAAAAAA A[gap/A]TAAAAG CAAATGCTAAAA ACTACTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3903	cg43935280	272	AAAAATTTTTTTTT TTTTTTTTTTTTC /TTCTGAGGAAG CCGAGAAACTTT AAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3904	cg43935280	444	ACCCAAGAGAG GCTGTGCGGCA GAG[C/gap]CCTG CACCCACAGGC CTTTGACAGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3905	cg43935280	446	CCAAGAGAGGCT GTGCGGCAGAG CC[C/gap]TGCAC CCACAGGCCTTT GACAGCAC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3906	cg43935280	530	TCACTCGACGCA CACCCGGTGCAT C[A/G]CACTGGC ACCTAAAGACAG GCCGTG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5

3907	cg44003023	7606	AAGCAAAGAGGAAAAACTTTGGACA[G/T]CGTAAAGACTAGAATAGTCTTTTAA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P40200 T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN) - Homo sapiens (Human), 569 aa.	9.9E-291	3
3908	cg44128920	1686	CGAGTCACGCTCAATTGAACCCTGC[C/T]AGAGACGGGAAGAGGGGGGCTGTCG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3909	cg44128920	1735	CGGCTGCTGCTTCTGGGCCACGGGG[A/G]GCCCCAGGACCTATGCACTTTATTT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3910	cg44128920	1749	GGGCCACGGGGAGCCCCAGGACCTA[T/G]GCACTTTATTTCTGACCCCGTGGCT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3911	cg44128920	1914	CATGTTTTACATCTTTTCTTTCTGC[C/gap]GCTCGGCTCCGGCCATTTTGTTTTA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3912	cg40886359	150	TCCCTCTCTGCAGAACTTCTCCTTT[A/gap]CCCCCCACCCCCCACCACTGCCCCC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18627 LYMPHOCYTE ACTIVATION GENE-3 PROTEIN PRECURSOR (LAG-3) (FDC PROTEIN) - Homo sapiens (Human), 525 aa.	1.6E-290	12 (12p13.32)
3913	cg42742569	3325	AAAAATGGATACCAAAAGCACTATT[A/T]GTCACCCAAGCTAAGTGGAATAGCT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O15091 HYPOTHETICAL PROTEIN KIAA0391 - Homo sapiens (Human), 567 aa.	2.5E-290	

3914	cg43949262	81	GTAGAGGCACAC ATTGGACTCTGA C[G/A]ATTCCCCT TGCAGCAGACAT TTGTG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
3915	cg43995003	1944	TTGCCATCAGTG ATCTCACTAAAA A[gap/A]TATACA GCTACTTCCCAG CTAATCT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
3916	cg43926814	360	AATAATTCAAAG TAGAATTTTCTAT [C/gap]CCCCCCC ATTTCTCCAGTA ATAAAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
3917	cg43926814	367	CAAAGTAGAATT TTCTATCCCCCC C[C/gap]ATTTCTC CAGTAATAAAAA GTAGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
3918	cg43931799	255	CCTATGTCGCGC CGGGCCCTCCG GA[G/gap]GCTGA GGGGGGAACAG CGCGGCCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA83001 KIAA1049 PROTEIN - HOMO SAPIENS (HUMAN), 550 aa (fragment).	7.6E-289	22
3919	cg43055270	2134	AAATATCAGAGT AAAACTTTCTAG A[A/gap]CAGTAC AAGGTTAAAGAG GTGAGGT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13884 BETA1-SYNTROPHIN - HOMO SAPIENS (HUMAN), 538 aa.	2.2E-288	8
3920	cg43055270	2305	GCCGAATAGTTG AGAAATGGACAT T[C/T]TTACCTAC TCCTCCTAGCCC CCTAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13884 BETA1-SYNTROPHIN - HOMO SAPIENS (HUMAN), 538 aa.	2.2E-288	8

3921	cg43969619	2350	TCACACACATGTCATCAGGGCCCTC[gap/C]TGCACTCCACATGATGAGGTCAGAC	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q00973 BETA-1,4 N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.92) ((N-ACETYLNEURAMINYL)-GALACTOSYLGLUCOSYLCERAMIDE) (GM2/GD2 SYNTHASE) (GALNAC-T) - Homo sapiens (Human), 533 aa.	2.5E-287	12
3922	cg43249686	1818	CCTCGCCCCCGCCCCCACCGGGTGA[A/G]AGTGTCGTCTCCGCTTCTCTCGGTG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q01101 ZINC FINGER PROTEIN IA-1 (INSULINOMA-ASSOCIATED PROTEIN 1) - Homo sapiens (Human), 510 aa.	1.4E-286	20
3923	cg43129343	1678	CACTTCTCTCCTCCACTCTGAGCCC[C/gap]CTGACCTTCCAAACCTCAATAAACT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3924	cg43129343	1679	ACTTCTCTCCTCCACTCTGAGCCCC[C/gap]TGACCTTCCAAACCTCAATAAACTA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3925	cg43129343	1921	CCTCTCCCCGCCGCTGCCATAACCC[C/gap]AATGTCTGGGCCCTGCGCAGCCCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3926	cg43968641	993	GTAATATAGGTGTGCACAAAAAGGG[A/gap]AAACACCCTATTTCATTTTTCAATT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3927	cg43968641	265	AAGTTAATTTTCTTTTCTAATTTCT[T/G]CTCATACACCTGAGTTATTTAAAAA	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8

3928	cg43968641	508	AGGACCAGTGAA GAATAGCTCCAA T[G/T]TGACACTA GACACAAAATAC CTTTG	G	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3929	cg43968641	555	TTTGGGGGCAAA GACAGGGGCAA GC[T/C]GTGTGC CGGTGGTGAAGT GAGAAGG	T	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3930	cg43968641	825	TTTTGACTCATG AGGCAAAGCTGT T[G/gap]CCACAA TCAGTGGCGACT CAAGTCA	G	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3931	cg43061073	119	AGCTATTTTAAAA CTAATGTAACCA[gap/T]TTTTTTTAA AAAAAGAAACTA TTTA	gap	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14117 DIHYDROPYRIMIDINASE (EC 3.5.2.2) (DHPASE) (HYDANTOINASE) (DHP) - Homo sapiens (Human), 519 aa.	8.6E-285	8
3932	cg43969352	296	GTTACAATTTAAA AAAAAGAATACA[A/T]CAGAATAAAT TAATAACTTAAGT GA	A	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60317 KIAA0571 PROTEIN - HOMO SAPIENS (HUMAN), 638 aa.	1.7E-284	11
3933	cg42709686	2604	GACAGTGATTAA TGGTTCTGTTGG C[C/gap]AAGGCT TCTCCCTGTCGG TGAAGGA	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N-ACETYLGALACTOSAMINE-4-SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
3934	cg43943490	2217	TGCCTGGGGTCA TGAAAGGCAGAG C[C/gap]TGCAGC ATGCAGTATGGC AGCCGGG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA10276 ARIADNE-2 PROTEIN (ARI2) - HOMO SAPIENS (HUMAN), 493 aa.	1.3E-281	3

3935	cg43946325	272	GATCCTAGCCTTGGGGCCAGGGATG[G/gap]CACAGGCTGAATGGAAGGGCTGGGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3936	cg43946325	65	GCTCTTTTTTTTTTTTTTTTTTTT[A/T]AGGCTTCTGGTAGGGACATTTTATT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3937	cg43946325	66	CTCTTTTTTTTTTTTTTTTTTTTA[A/T]GGCTTCTGGTAGGGACATTTTATTT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3938	cg44010409	223	CTCCAAATCCCACCCCAGTGCAAGT[C/T]TGGGGAAGGTAGGGTGTGAGCTGCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
3939	cg44010409	239	AGTGCAAGTCTGGGGAAGGTAGGGT[G/T]TGAGCTGCTGCTGAAGGCTGTCCCC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
3940	cg43931431	1146	CTTCTTGTGAACCAGGGATACACAC[A/T]TCAGACATTGGCAAACAGTAGTACA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5
3941	cg43931431	320	ACATAAAATTGCAGTATGAACTGAT[G/T]GACAAGAACTCTGGGCCAGGAGTCA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5

3942	cg43930921	329	CCGGAGCTCGC CTTGGTGCTGGG CA[C/gap]CAGTG GGCCCCTGCCA GGCCTGTCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3943	cg43930921	330	CGGAGCTCGCC TTGGTGCTGGGC AC[C/gap]AGTGG GCCCCTGCCAG GCCTGTCCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3944	cg43930921	340	CTTGGTGCTGGG CACCAGTGGGC CC[C/gap]TGCCA GGCCTGTCCTCT CCTTTTTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3945	cg43930921	344	GTGCTGGGCAC CAGTGGGCCCC TGC[C/gap]AGGC CTGTCCTCTCCT TTTTGAGCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3946	cg44931278	33	TTTTTTTTTTTTT TTTTTTTTTTTTA /T]ACTACAAAAAT AAGCACTTTACT AA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
3947	cg44931278	34	TTTTTTTTTTTTT TTTTTTTTTTTA[A /T]CTACAAAAATA AGCACTTTACTA AC	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
3948	cg43998884	2376	GGCAATGCCCGT CCTCTGGCTTGG G[T/C]TAATTCTT CGGTGACACTG GCGTTG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51688 N-SULPHOGLUCOSAMINE SULPHOHYDROLASE PRECURSOR (EC 3.10.1.1) (SULFOGLUCOSAMINE SULFAMIDASE) (SULPHAMIDASE) - Homo sapiens (Human), 502 aa.	1.1E-279	17

3949	cg4398884	2629	CCATACTGGGGT GGGCTGGAGGA GG[gap/C]CACAG GCCAGCTATTGT AAAAGCTT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51688 N-SULPHOGLUCOSAMINE SULPHOHYDROLASE PRECURSOR (EC 3.10.1.1) (SULFOGLUCOSAMINE SULFAMIDASE) (SULPHAMIDASE) - Homo sapiens (Human), 502 aa.	1.1E-279	17
3950	cg43956499	2184	GTCTGGCAATTT TGATTTCTGAAC T[C/T]TGTGCTAC CTCAGAGGCCA GCTTCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75686 2'-5' OLIGOADENYLATE SYNTHETASE (P59OAS) - HOMO SAPIENS (HUMAN), 514 aa.	2.2E-279	12
3951	cg44001088	178	TCCACCACAGTA AAACATACAAGT T[T/A]TTTGCAAG AGAAAAGGTCAT ATGGA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
3952	cg44001088	179	CCACCACAGTAA AACATACAAGTT T[T/A]TTGCAAGA GAAAAGGTCATA TGGAT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
3953	cg44031765	1170	ATTCACCTCAAG TCAGGTGAGACC C[A/G]TACATCAT GGGTCCCCACTC ACAAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22
3954	cg44022026	1864	TCCTTCTGGGGA AATAAATGAGTG T[C/gap]TGTTTCA GCAGCTAAAAAA AAAAAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43292 HGAA1 - HOMO SAPIENS (HUMAN), 621 aa.	1.2E-278	8

3955	cg44002920	142	AGCACAGTTCAA AGTCATTAAATC C[G/A]GTACAAAA GAAATGGCTCTC ACTTC	G	A		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3956	cg44002920	171	AAAAGAAATGGC TCTCACTTCCTG G[gap/G]ATTGGC ACCAGACATCCT ACCAGCT	gap	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3957	cg44002920	176	AATGGCTCTCA CTTCCTGGATTG G[gap/G]CACCAG ACATCCTACCAG CTGCAAT	gap	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3958	cg43987191	1808	ACTCAAGACTTA TGGAACAGGGAT G[G/gap]CGAGGC CTCTCTCAGGAG CAGGGGC	G	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P19235 ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R) - Homo sapiens (Human), 508 aa.	8.5E-278	19 (19p13.3)

3959	cg43984386	281	ACGAGCTCTCGC CCACTCGCCGG AG[G/gap]AGACG GCCCTGGACTCC CAACCCCG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00401 N-WASP - HOMO SAPIENS (HUMAN), 505 aa.	5.9E-277	
3960	cg43963979	502	GATAGAAGGGA GCAGCATCAGAC AC[A/T]TTTTTTC AGGCCCTGGTTT CATGTG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3961	cg43963979	503	ATAGAAGGGAGC AGCATCAGACAC A[T/A]TTTTCAG GCCCTGGTTTCA TGTGC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3962	cg43963979	504	TAGAAGGGAGCA GCATCAGACACA T[T/A]TTTTCAGG CCCTGGTTTCAT GTGCC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3963	cg43963979	505	AGAAGGGAGCA GCATCAGACACA TT[T/A]TTTCAGG CCCTGGTTTCAT GTGCCT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3964	cg43963979	582	TATTCACTAAAC AATTTTTTTTTTT[T/gap]TGTAAGGC TACTTTTGTAGC TTTTT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3965	cg43963979	583	ATTCACTAAACA ATTTTTTTTTTT[T/gap]GTAAGGCT ACTTTTGTAGCT TTTTG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14

3966	cg43963979	702	CAATTCAATTCG TTGCCTTTTGAG G[C/gap]CACTGT GGCCATGAACAG CCCTGCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3967	cg43963979	712	CGTTGCCTTTTG AGGCCACTGTG GC[C/gap]ATGAA CAGCCCTGCTAC TATCTGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3968	cg43988211	104	CAATTCCAGAGG GGCCTGGCTGT GG[C/gap]CAAAG CTGTGCCAAACG GTTGGGAT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3969	cg43988211	105	AATTCCAGAGGG GCCTGGCTGTG GC[C/gap]AAAGC TGTGCCAAACGG TTGGGATC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3970	cg43988211	182	TGAGACCATGGG CGAGGCTCCCC AC[G/A]CTATCTC CACCACCACAGT CATGAG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3971	cg43988211	302	CTCATCCTGAGA GGCATTGGGTG CC[C/gap]ACTCA CTGGCTGGATGC TGGGCTGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3972	cg42935995	134	TGACCTTGCACC ATAATTATGGTG A[G/A]TTCTAGG TTAGAAGATACC TTAGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1E-274	

3973	cg42935995	484	ACTGGGTTAGCT GGATTTTGTCCT T[G/gap]AGCTTT GAGAAGGCCTA GTTCTCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1E-274	
3974	cg43929467	1829	AAAGACAAGGA CTGCTCTAGTGT T[G/C]AGGGATG TAGCTCAGCTTT TGGGCT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3975	cg43929467	2628	CATCTCAAAAAA AAAAAAAAGCGG G[T/gap]GGGGGG GAGTTGGGCTGT GTTGGAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3976	cg43929467	2733	TTGCTAGGTCAG AATGAGAGACTG G[T/A]GGTCTGT CTACCTGTTTCT TCTAC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3977	cg43947753	3093	TCATTGGTGTAG CAACGTGGGTTC A[C/gap]CCAAAA CACCTTTTTATAC AAAAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.1E-274	12
3978	cg43947753	3095	ATTGGTGTAGCA ACGTGGGTTCAC C[C/gap]AAAACA CCTTTTTATACAA AAGACA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.1E-274	12

3979	cg43994885	55	TTTTTTTTTTTTTTTTTTTTT[T/C]TTTTGTTGACAAATGTTGTTTATTG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43147 KIAA0397 - HOMO SAPIENS (HUMAN), 488 aa.	1.2E-272	17
3980	cg43333012	406	TCAGCTCCCTCTTCTTGGTATTACA[A/G]AATTTCATACTTATCCACTAGGAAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272	11 (11q23.3)
3981	cg43328330	1629	CTCTCGCCTTCCAGCAATTCCCCGC[A/gap]GTGCTACAAATGGGAAGTCAGAGAC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16222 UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) (ANTIGEN X) (AGX) (AGX-1) (SPERM-ASSOCIATED ANTIGEN 2) - Homo sapiens (Human), 505 aa.	5.5E-271	1
3982	cg43970492	169	TCTATAAGATGTATCTCCCCAAAGA[T/G]CACATTAACTCCTCAAGTCAACATC	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3983	cg43970492	201	AACTCCTCAAGTCAACATCTGCCTA[T/C]CCCCAACTTCCCCTTTTTTTCCTCA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3984	cg43970492	391	AGCATTTGATATGTGCACCCAGCTA[G/A]TTAGGCATGAAACAGGGGCACAGGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3985	cg43958878	1627	GAACGCGAACTGTGCCATGGGAGCG[C/gap]CCGCAGGGGGAGGAGTCCTTGCAGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9

3986	cg43958878	1641	CCATGGGAGCG CCCGCAGGGGG AGG[A/G]GTCCTT GCAGTTGGTGCC TACGGAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
3987	cg43958878	1659	GGGGAGGAGTC CTTGCAGTTGGT GC[C/gap]TACGG AGCCCGTGCCCT CCGGAGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
3988	cg43926574	2586	AAATTAAATTGG ATATTAAATTGTA [A/T]AGACATCAT TTATTAATTTTAA ACT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.1E-268	7
3989	cg43926574	3018	TATTAACCTGCC CTTTACACAAAA T[C/T]ACACAAAA AGTTTCCTGATC TCTGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.1E-268	7
3990	cg43927211	29	TTTTTTTTTTTTT TTTTTTTTTTA[A /T]GCCAGAGGTG AGATCTTTATTG ACT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15057 HYPOTHETICAL PROTEIN KIAA0041 - Homo sapiens (Human), 632 aa (fragment).	1.3E-268	3
3991	cg43951018	86	TTTTTTTTTTTTT TTTTTTTTTTT[T/ A]TTGCTTCACTG CTTTATTTTTGAA A	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16851 UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE 2 (EC 2.7.7.9) (UDP- GLUCOSE PYROPHOSPHORYLASE 2) (UDPGP 2) (UGPASE 2) - Homo sapiens (Human), 507 aa.	1.8E-268	2

3992	cg43326821	251	GGCTAACCTTGCCGCGGGCCGAGCC[C/gap]TGCCTCGCCATGGACCAGGACTATG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75869 R33374_1 - HOMO SAPIENS (HUMAN), 493 aa.	6.1E-268	
3993	cg43949042	268	GGAGAGGTGGGCTCTGGCAGCGGGT[G/T]TGAGGTGGCAGTGAGAAGCCAGGCC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa.	6.1E-268	
3994	cg44022853	30	TTTTTTTTTTTTT[T/A]AGCAATTGTTTTATGTTTAATTTAC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12891 LYSOSOMAL HYALURONIDASE (PH-20 HOMOLOG) (LUCA-2) (LUCA2) - HOMO SAPIENS (HUMAN), 473 aa.	2.1E-267	3
3995	cg43031103	742	CTTCAAAGTAGCCTGCTGGAGCCT[T/A]GATCATCAGAGGATGTTCATCAGAG	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.3E-266	
3996	cg42919561	363	GGTGACTCTGGAGTTCTTGAGGGGC[G/T]CCGTGCCCTGACTGTGGATGTGAGC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00515 LADININ - HOMO SAPIENS (HUMAN), 517 aa.	7.2E-265	
3997	cg43313186	2105	GTTTGTTTTTCCCCTCAGCCCTGCC[A/C]CCGTGGGGAGTCTGGTTTTTCTCTT	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
3998	cg43313186	2196	GCCTGTGAGCACCACAGGCAGCCCGG[C/A]CCAAAAAAAAAAAAAAAAA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)

3999	cg4313186	2197	CCTGTGAGCACA CAGGCAGCCCG GC[C/A]CAAAAAA AAAAAAAAAAA AAAAAA	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
4000	cg43942622	1782	GGGAGCGGCAA GGCAGGGCAGG CGG[C/gap]CCCA GGAACCTGCCCA GTGCACAGG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4001	cg43942622	297	CATAAAAATATC ACCTCAACTCAT C[C/G]CTGACAC ACGCATGTCCTC CCAAGG	C	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4002	cg43942622	41	TTTTTTTTTTTTT TTTTTTTTTTT[C /T]TGTGCACAAA AATGATACATTTA TT	C	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4003	cg43942622	582	GAAAGCCACCCA TAAGCCCCAGCT A[gap/G]TCTCCA GGAGAAAGCCC AGAAAGGT	gap	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4004	cg43934408	326	CACACCAGGCC CTGCTCTGCCGC AG[G/gap]AAAAT GGATTCCCAGGC CACAGAGC	G	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4005	cg43934408	369	CACAGAGCTGTC AGGCCTTTGACT T[T/C]GCAGAGAC CAAGCACCCCAG AGGCT	T	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22

4006	cg43934408	715	ACCCTTCTCCTA TGCCTCCCAGG GT[gap/T]ACTGT GTCTCAAAGAAC CTCTTCCC	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4007	cg43934408	729	GCCTCCCAGGG TACTGTGTCTCA AA[G/gap]AACCT CTTCCCTCCTGG GAACCATT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4008	cg43934408	729	CCTCCCAGGGTA CTGTGTCTCAAA G[gap/G]AACCTC TTCCCTCCTGGG AACCATT	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4009	cg43934408	745	TGTCTCAAAGAA CCTCTTCCCTCC T[G/gap]GGAACC ATTTTCCACTCC TCTTTCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4010	cg43934408	747	TCTCAAAGAACC TCTTCCCTCCTG G[G/gap]AACCAT TTTCCACTCCTC TTTCTTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4011	cg43980328	183	AAGACTCATGAA GTATAATCTCTC A[T/C]CTTCTTTC TCTTTCCCCTGC CCAAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4012	cg43980328	207	ATCTTCTTTCTCT TTCCCCTGCCCA [A/G]CCCTAAGT TAGGGTTCCCAT CCAT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

4013	cg43980328	273	GGTCAGGTGGC ATTTGCTATCTCT G[A/G]GATTCCCT GCCCATGAAAGC CACAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4014	cg43980328	385	AAACTGTGGTTT AAAAACAAAACA A[A/C]CCAACCAC TGTGAAATATTTA TTTT	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4015	cg43980328	455	TGATTAAACCAG TGCAGAAAAATA C[C/T]AAGTACAT TGGGTGAACGAT GAGCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4016	cg43980328	469	CAGAAAAATACC AAGTACATTGGG T[G/A]AACGATGA GCTAGCTGTTCT AGTAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4017	cg43980328	523	CTTTTTGTAATCC AGTTAAGACCAT[C/G]AGCATATAC AACATCATCACT AACT	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4018	cg43980328	535	CAGTTAAGACCA TCAGCATATACA A[C/T]ATCATCAC TAACTCAACAAT GTAGC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4019	cg43980328	572	CTCAACAATGTA GCTGCAGGGTAA C[A/C]TGTGGATA CCCTGTGTGCTC TACTG	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

4020	cg43056973	129	GAGTGCCTCAGCAGCTTCTCCACAT[G/C]CTCTTCAGTCCCCAAAGTTGGAGAA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20711 AROMATIC-L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DECARBOXYLASE) (DDC) - Homo sapiens (Human), 480 aa.	5.2E-262	7 (7p11)
4021	cg43922182	2206	CCTCCTTTTTCGGTTTCCTCTTGTC[gap/T]TTTTTTTTTTATTTTTATTACGAAG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF-RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
4022	cg43922182	2216	CGGTTTCCTCTTGTCTTTTTTTTTT[gap/T]ATTTTTATTACGAAGTTTCATTCTT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF-RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
4023	cg44013054	271	TACACACACACACACACACACACAC[A/gap]CTTACACACATGCACACATCCTAAG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P15391 B-LYMPHOCYTE ANTIGEN CD19 PRECURSOR (B-LYMPHOCYTE SURFACE ANTIGEN B4) (LEU-12) (DIFFERENTIATION ANTIGEN CD19) - Homo sapiens (Human), 556 aa.	3.3E-261	16 (16p11.2)
4024	cg40296063	103	AGCCCTATGGGTGGGGATGGCACCG[C/gap]CCTACCGCCGAGAGAGTTGAAGCTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O94810 REGULATOR OF G-PROTEIN SIGNALING 11 (RGS11) - Homo sapiens (Human), 467 aa.	3.3E-261	
4025	cg43971058	1035	CATTAGTAACATAACTCAACATCCT[T/C]AATTTGGTATAGATGTGACACATTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60455 POLYADENYLATE BINDING PROTEIN-INTERACTING PROTEIN-1 - HOMO SAPIENS (HUMAN), 480 aa.	3.7E-261	
4026	cg27359628	100	TTCCCATGCCCCTCCCACGGTCAGC[A/T]CCCCGATGGCCTGGGTGAGGGCTGA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	

4027	cg27359628	123	GCACCCCGATG GCCTGGGTGAG GGC[T/A]GATAG GCTGCTCTGACA CCATGGGG	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260
4028	cg27359628	125	ACCCCGATGGC CTGGGTGAGGG CTG[A/G]TAGGCT GCTCTGACACCA TGGGGAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260
4029	cg27359628	76	ACAAGGGGAATA AGTGGGACCCT T[T/C]CCCATGCC CCTCCCACGGTC AGCAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260
4030	cg43916582	242	AACAGTTATCTC AGAGGGTCAACC A[C/T]ACAATGTC ATACAGAGACGC TGGTC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75475 LENS EPITHELIUM-DERIVED GROWTH FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	2.3E-259
4031	cg43980777	364	TCTTTTGAGGCT TTACAATTACAAA [T/C]GACAATGAT GTCAACCCATTT ATCA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259
4032	cg43075307	103	GTATAGACCAAC ACTGTCCAACCA A[T/C]AGAACTTT CTGCCATGATGG CATAT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60623 DIPHTHAMIDE BIOSYNTHESIS PROTEIN-2 - HOMO SAPIENS (HUMAN), 489 aa.	1.3E-258
4033	cg43075307	90	GAAATAAGAGTC AGTATAGACCAA C[A/G]CTGTCCAA CCAATAGAACTT TCTGC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60623 DIPHTHAMIDE BIOSYNTHESIS PROTEIN-2 - HOMO SAPIENS (HUMAN), 489 aa.	1.3E-258

4034	cg43258841	140	GAAATACATTCT TTTCACATGATA A[T/C]GTTTTCGC CCTTATTTATGG TCTTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.7E-258	
4035	cg43999171	48	TTTTTTTTTTTTT TTTTTTTTTTTT[A /T]TTACCAAACC CAACATTTATTG AGA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	3.8E-257	6
4036	cg43255855	1805	TAAGCTAAAAAA CAGGCTGAAAAA G[G/A]AATTCCCA AAGAGAGTTAAC AAAAC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43148 KIAA0398 - HOMO SAPIENS (HUMAN), 476 aa.	1E-256	18
4037	cg43918866	1419	CCTCAGCCTCCC AAGTAACTGGGA A[T/C]ACAGGTAC CCACACCCACAC CCAGC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15519 CASPER - HOMO SAPIENS (HUMAN), 480 aa.	3.5E-256	2
4038	cg43963125	1099	TAGAGGAAAACT GTAATATAAATG C[gap/A]TTTTTTT TTTTTTGCTTTTA AAGGA	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20
4039	cg43963125	403	GGGTCTAGTACA GAATAGACAGTA A[A/T]TCTTTGTT GAAAGAACTCTT TTATT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20
4040	cg43963125	563	TCAAGACTTTGC TCACTAGTCAGA C[C/T]GTAATTTT TAGAAGGAATAG GAGCA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20

4041	cg43949732	1699	TGAAGAACTGAA GGAGTCCTGCAT C[T/gap]TTTTTTT TTTATCTGCTTCT GTTTA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4042	cg43949732	1709	AAGGAGTCCTGC ATCTTTTTTTTTT[T/gap]ATCTGCTT CTGTTTAAAAAG CCAAC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4043	cg43949732	1709	AGGAGTCCTGCA TCTTTTTTTTTT[gap/T]ATCTGCTT CTGTTTAAAAAG CCAAC	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4044	cg43949732	1828	GTTTTAGTTCCTT ACAAACAGGGTT [G/gap]GGGGGG GGAAGGGCGTG CAAAAACT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)

4045	cg43949732	1836	TCCTTACAAACA GGGTTGGGGGG GG[G/gap]AAGGG CGTGCAAAAACT AACATTGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4046	cg43274303	746	ATTGGGACCACC GGCTGGTGGTG CA[G/T]GTCCAGA ACATTCTGGGGG CTGCAG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15175 PARANEOPLASTIC ANTIGEN - HOMO SAPIENS (HUMAN), 535 aa (fragment).	7.6E-254	17	
4047	cg43943285	1459	ATTGACCCACAA AGTTTCAGAAAT T[T/C]TCTGAAAG TTTCTTCCTTTTT TCTC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P04469 FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA') - Homo sapiens (Human), 453 aa.	4.2E-253	4	
4048	cg43971614	736	CCTTTATCAAAA AAAAATTCTATTC [C/T]TTTTATTCA GTTTTTAAACATA CCA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.3E-253	5	
4049	cg43040311	560	ATGGAATAGATT TTGCCAAACCTC A[C/T]TGCATATT TACAGTATTTTAA GCAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q00425 PUTATIVE RAS INHIBITOR - HOMO SAPIENS (HUMAN), 471 aa (fragment).	5.3E-253	20	
4050	cg43040311	84	TTATGTGCAAAA TTCCATTTAAAAA [A/gap]TCATTTAC AAAAGTACAACA CAGTA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q00425 PUTATIVE RAS INHIBITOR - HOMO SAPIENS (HUMAN), 471 aa (fragment).	5.3E-253	20	
4051	cg44034555	386	GAAGTGAGGGC CCAAAATAGGGA GT[G/T]TGGGTG ATGAGGGTGGA GTTCAAAT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1	

4052	cg43962954	103	CTGAGTGTCACG GGGCCAGGGGA AG[G/gap]CTGGA GCCAAAACCAAG TCTCTGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4053	cg43962954	110	TCACGGGGCCA GGGGAAGGCTG GAG[C/gap]CAAA ACCAAGTCTCTG GGGGCGGGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4054	cg43962954	111	CACGGGGCCAG GGGAAGGCTGG AGC[C/gap]AAAA CCAAGTCTCTGG GGGCGGGGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4055	cg43962954	211	TAGAGACGGGA GAAGTCCAGTGT GC[T/C]GTTCCAC CTCCCTCCAAGT CCCAAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4056	cg43962954	328	AGGCCGGCGTG GTCAGGTCGGG GGC[G/A]GGAGG GCCGGGCCTGG CTCTGTCTC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4057	cg43962064	213	CTGTCAACCTTT TATTGGGAGTGG A[A/gap]CACATG AGGTTCAGCTCG TGCCGGG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20

4058	cg43962064	305	ACACTGACGCCA CACTGAGCAGGA T[G/gap]CACGGC CCGGGGCTCAC ACTGTCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4059	cg43962064	420	GGGACTGTGGC TCAGCTGACCCG TG[G/gap]CACAG CTGCACCTAAGA CATGGCCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4060	cg43962064	461	GACATGGCCCTG GCTAGGCGGGA AC[A/G]GCTCACA GTAGCGATACAT TCACAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4061	cg43962064	487	GCTCACAGTAGC GATACATTCACA G[G/gap]ACACAG TTGGTGTCCAGA AAAGGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4062	cg43962064	620	CAGCAGCTCATG CCCGGCATCCG CC[C/gap]ATGCT GGGAGACTCCCT GAAAGGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4063	cg43962064	647	TGCTGGGAGACT CCCTGAAAGGTG G[G/gap]CACCTG CCGTCTATGAGG AGGTGTC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4064	cg43924291	1180	ATATGCTTTAAG ACGCTTTCGTCC A[T/gap]TTCATAC CGCTCATTCTCA AGCGCC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	

4065	cg43924291	1182	ATGCTTTAAGAC GCTTTCGTCCAT T[T/gap]CATACC GCTCATTCTCAA GCGCCAC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	
4066	cg43924291	1182	TGCTTTAAGACG CTTTCGTCCATT T[gap/T]CATACC GCTCATTCTCAA GCGCCAC	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	
4067	cg42300443	318	TGGTGGAGCTTT GGAGCTGAGGC GG[G/gap]CAAGG CCTCTCAGATGG TCACGCTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P55249 ARACHIDONATE 12-LIPOXYGENASE, EPIDERMAL-TYPE (EC 1.13.11.31) (12-LOX) - Mus musculus (Mouse), 662 aa.	6.5E-249	
4068	cg44027341	2085	ATTGTACCTAAG TAAATTTTCTTTA [A/G]GTCAGAAG CCCATTAAAATA GTTAC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00439 PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4-MONOOXYGENASE) - Homo sapiens (Human), 452 aa.	1.6E-246	12
4069	cg43996564	127	CAAACTCAGTAG GAGTGCAAGGG CT[G/A]TACCCCC GGAGCTAGACA GCCTGGG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
4070	cg43996564	402	ACCTTGCCAAGT AGATGCATATGG A[gap/G]CATGGA ATGAATGGTGTC TGCTGTG	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
4071	cg43996564	405	CTTGCCAAGTAG ATGCATATGGAC A[T/gap]GGAATG AATGGTGTCTGC TGTGGTT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3

4072	cg43980318	1501	TGAGAGGGAGG GGAAAAGACTTT CT[T/gap]AAATAT TTCATTTATGAC CTGCAAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4073	cg43980318	1529	ATATTTCATTTAT GACCTGCAAATT[T/C]AAGAATAAA GACACTGAAGTA AGTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4074	cg43980318	1561	AAGACACTGAAG TAAGTTTGAAGC C[gap/T]CTACAG TTGTTTCCAGTC TTTTCAG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4075	cg43980318	1700	CTCTCATGGTGC CACGTTTTTTTTT [gap/T]CAATGTTT AGTAATAGTATA ATCCA	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4076	cg43980318	1700	CTCTCATGGTGC CACGTTTTTTTTT [gap/T]CAATGTTT AGTAATAGTATA ATCCA	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4077	cg43965612	131	CAGTAGCTGAAG GGGCCTGAGCA GA[G/gap]CTGGT GCTGGGAGGGG CCGGCATGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O43236 BRAIN PROTEIN H5 (PEANUT-LIKE PROTEIN 2) - Homo sapiens (Human), 478 aa.	6.9E-244	17
4078	cg43920589	1996	TTTATATCACTGT TTTTCACTGTTT[T/C]TGTGGACAA ATAATGGTTGCT TTGC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18

4079	cg43920589	2080	ACCTACCCAAAA GCTGTAGTCACA C[G/A]TCCTAAAG GCCAAGCAAACC CACCG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18
4080	cg43920589	2104	CGTCCTAAAGGC CAAGCAAACCCA C[C/T]GGGATGG TGGGGGGTCTT GGAGCCA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18
4081	cg43985156	167	GGTGACGGGCT CCGGGCTCCCG AGG[T/gap]GAAG AGCATCGGGGG CTGAGGGATG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.8E-243	17
4082	cg43985156	1811	CTTTCTTCTCTG AAAAAAACTAATT [T/A]AAATTTGCT TTTCTTTTTTTTA ACT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.8E-243	17
4083	cg43315249	146	CATTTAACTCCC CAGGTTAAACAC C[T/C]TGTAATTT ACCTTGAAGCTC TTTAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45712 HYPOTHETICAL 63.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 564 aa (fragment).	2.7E-242	17
4084	cg43315249	303	ACTTCAGAGAAA AATCCCAGATGA C[G/A]GCACTGG ACAGGTTATAAA GAGTTC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45712 HYPOTHETICAL 63.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 564 aa (fragment).	2.7E-242	17
4085	cg43292372	786	AGCCCTTGGGAA GCCCATCTCAGG G[G/A]GATCCAG GAGCAGATGGC CAAAAA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14740 SMAD7 PROTEIN - HOMO SAPIENS (HUMAN), 426 aa.	1.5E-241	

4086	cg44021361	109	TTATTTGGAAGG GCAGAGTCCAAC C[C/A]ACCCCAG GTCCTGAGGGTA GACTCA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
4087	cg43917689	1962	CAGGGCCAAGA GCGCCTCACAAA GG[G/gap]CTGCT GCCTTGAACTTG GCCTGGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.5E-240	3
4088	cg43976131	1814	GCGGAATGGGA AGCAGTTTATGG AG[T/C]TAAGTGG GGCTCTGCTATT TCCCCC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4089	cg43976131	1888	TTCCAGGGCAGA GTGAGGGGCAG AC[G/A]GGATGA GGCTCTTCTGTA AAGTCCA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4090	cg43976131	199	CGAGGCAGGGT CCCCAAGTGGA GGC[G/A]GGGCG GGACGTGAGAG GATGGGGGC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4091	cg43928134	204	ATTCAAATGGAA ACAGACAATTTA A[C/A]AAAGAGAA GTAAAAAAATTTA TTGC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4092	cg43928134	208	AAATGGAAACAG ACAATTTAACAA A[G/A]AGAAGTAA AAAAATTTATTGC AGTA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8

4093	cg43928134	210	ATGGAAACAGAC AATTTAACAAAG A[G/A]AAGTAAAA AAATTTATTGCA GTATT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4094	cg43928134	213	GAAACAGACAAT TTAACAAAGAGA A[G/A]TAAAAAAA TTTATTGCAGTAT TCGC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4095	cg43981846	1430	AATATGTGTTGT ATGTCTTTTTTTGC [T/gap]TTTTTTTT TAAAAAAAAGAA TAACT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD33924 LOMP PROTEIN - HOMO SAPIENS (HUMAN), 797 aa.	1.2E-239	13
4096	cg43981846	1439	TGTATGTCTTTTT TGCTTTTTTTTTT[T /gap]AAAAAAAAG AATAACTTTTTTT GCC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD33924 LOMP PROTEIN - HOMO SAPIENS (HUMAN), 797 aa.	1.2E-239	13
4097	cg43950654	1462	ACTGAAGAACCA TAAAGAAAAGAT G[A/gap]AAAAA AAACTATCAAAG AAAGATG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
4098	cg43950654	1471	CCATAAAGAAAA GATGAAAAAAAA A[A/gap]CTATCAA AGAAAGATGAAA TAATAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
4099	cg42750618	85	GCCAGGTTATAC CCTAGGACGGT GT[C/gap]CTTCC CTCCCTCCTAGG GTGGGAGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	2.9E-238	1

4100	cg43922856	1099	AGTTGAACGTGC CAAAGAGATACC A[T/C]TCAGTTGG ATTTTCTAGGGT CAACA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2E-237	12 (12q22)
4101	cg43923262	1651	GCTAATGGCGAT CATCTTTGCCAC C[A/G]CCTGGGG AGAGCCTGCTTG GGAATG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15527 8-OXOGUANINE DNA GLYCOSYLASE 1 (EC 3.2.2.-) - HOMO SAPIENS (HUMAN), 424 aa.	4.8E-236	3
4102	cg41637661	54	TGGGCCGCCAG ACTCGGGAGAG GCT[C/G]CGTCTT GTGCAAGGGTC CTGTGGGC	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O43913 ORIGIN RECOGNITION COMPLEX SUBUNIT 5 - Homo sapiens (Human), 435 aa.	6.1E-236	
4103	cg43932322	52	TCTTTTTTTTTTT TTTTTTTTTT[G /T]ATTTTTTTTTG TTTTTTCCAATTT A	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O88941 GLYCOPROTEIN PROCESSING GLUCOSIDASE I - RATTUS NORVEGICUS (RAT), 834 aa.	6.5E-236	2
4104	cg43933215	299	GTCCTCCCCAGC CAAGTCAGGTGC C[C/T]AGCCCAG ACCCTGCCCTGG CAAGGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	1.6E-235	5
4105	cg43330158	1507	ACCTGAGCCACC CTCAGCAGGAG CT[G/gap]GGGTG GCCCCTGAGCTC CAACGGCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
4106	cg43957219	3538	GAGAGGAACATT CCATTTATTTGTA [G/T]TGGATTTCC TCTGGAGGGCAT GTAC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00345 HSP1-A - HOMO SAPIENS (HUMAN), 452 aa.	4.3E-235	X

4107	cg43955823	317	CTTATCTGTTCA AATATACCTGGA A[G/A]GGAAATAC ACAGAGGGTTCA GCAGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05048 CLEAVAGE STIMULATION FACTOR, 50 KD SUBUNIT (CSTF 50 KD SUBUNIT) (CF-1 50 KD SUBUNIT) - Homo sapiens (Human), 431 aa.	5.5E-235	20
4108	cg43930174	1732	GTGGCAGGACT CGTGGGCCCTCT CC[G/A]GCCTGTT TCCCCTGCCACT CCAGCC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
4109	cg43930174	275	CCTGTGGGACC GTTCCTCCTAGC CC[G/T]GTGGTTT GGAACCAGTGG CTTTGGG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
4110	cg43948360	432	GCAAGGCAGCG GAGGGGCAGTG GGG[C/gap]CCCA GCATCCCCTGAA GCCTCACCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
4111	cg43948360	435	AGGCAGCGGAG GGGCAGTGGGG CCC[C/gap]AGCA TCCCCTGAAGCC TCACCTGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
4112	cg43962127	205	TCAGATCAGCAG ACCGAGTCGAAA T[G/C]TGATTCTT CAAAGCAAGTAT TGCTT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4113	cg43962127	253	CTTTACCCTTGT CCTGAATGCAGT C[C/T]GTCATATG ACCACTAACTTG CATGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7

4114	cg43962127	270	ATGCAGTCCGTC ATATGACCACTA A[C/T]TTGCATGT GACCAAATGTTT GCAGA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4115	cg43962127	317	CAGAGTGTTTTT TAGATATGCTCT C[G/A]GTGAGCC GTCATCCGTCAA TCCAAG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4116	cg43962127	97	GTCTTATTTTCCA GTAAAATATTCA[C/A]ATAATGTCA AAAGAATGAAAT GATA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4117	cg43952917	525	TCTTACTTTGGC AAGAGAAAACAG A[G/A]GTATTTTT GCTCCTCTTCTA CCCAA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q99611 SELENIDE,WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2) - Homo sapiens (Human), 448 aa.	1.5E-232	
4118	cg43940463	220	AAGAACCACTCC TAGCCTCCGCAG G[G/gap]CTCTTT TGGGAACCCCTC CCTGCTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.1E-232	
4119	cg43966506	2018	TCACCATGTTGG CCAGGCTGGTCT C[G/A]AACTCCTA ACCTCAGGCGAT CCACC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92966 SNRNA ACTIVATING PROTEIN COMPLEX 50KD SUBUNIT - HOMO SAPIENS (HUMAN), 411 aa.	8.3E-232	9
4120	cg43966506	2914	AGGTCTAGACCA TCAGATAGATTT A[C/T]TCAAATAT TTTCTGGGAACC TTTAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92966 SNRNA ACTIVATING PROTEIN COMPLEX 50KD SUBUNIT - HOMO SAPIENS (HUMAN), 411 aa.	8.3E-232	9

4121	cg43983092	127	TAGCTAATTATTTACAAACTCATTT[T/gap]AAAGACTAGAATTTTAAATCGAAGG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD29607 HYPOTHETICAL 53.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 448 aa.	1.7E-231	1
4122	cg43983092	922	TCCTGGTTTCCTTTTTTGGCCCCGC[C/gap]ACAGAAAAGATGGATGTAGTAAGAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD29607 HYPOTHETICAL 53.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 448 aa.	1.7E-231	1
4123	cg43947107	420	GACCAAGCAGAGACTAGGCCTCAGG[C/gap]TAGCCCAGCAGGGCTTCCTGTGTCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75528 ADA3-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 432 aa.	2.8E-231	3
4124	cg43948144	1510	TAATATGTTTATTAGTTCTCTTTGG[A/gap]AAAAAACTACCACTGTGGTCTTAAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
4125	cg43948144	1541	ACTACCACTGTGGTCTTAAAAGGGA[G/A]CAAAATATACCATAGGCTAAAACTA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
4126	cg42676981	426	CCGAGACAGGTGTGCATGGTGGGTG[C/gap]CCCCTGCTGATGGTGTGAGGTCAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15
4127	cg42676981	544	CTGCTGGAGCGTGCCAGAGTCCGGA[G/gap]GCCTCACTCCAGGTCGGCCTCCACC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15

4128	cg42676981	545	TGCTGGAGCGT GCCAGAGTCCG GAG[G/gap]CCTC ACTCCAGGTCGG CCTCCACCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15
4129	cg43968343	1175	TACATTGAGGAA AGTGAGATTCAC A[gap/G]CACAAA TACCAAGATGAC CAATGAA	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4130	cg43968343	1420	CAGAGGGGACT CTCCGTACCCTT TC[A/G]GGAGGG TTTTGGGCAATA AAGCCAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4131	cg43968343	1453	TTTGGGCAATAA AGCCAAAATCTG T[A/G]CTTAAATA GGTGTGTCTCAT AAGAC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4132	cg43968343	1488	GTGTGTCTCATA AGACAAATTTTTA [A/G]CTCATTTAT TAAAGGTCCTGA TGGA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4133	cg43968343	1508	TTTTAACTCATTT ATTAAAGGTCCT[G/A]ATGGACATT CCAAACTAGTAA CTTA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)

4134	cg43968343	1750	TGCCTAACGCCA CGGGGTCCACC GG[T/C]GGGGGT CACAGCTGCTGG CTGGTGA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4135	cg43968343	546	GGAGGAAAGAG AAAGTGATCTTT AC[T/A]TTTTTTTC ATGGAACCACCG GGGAT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4136	cg43968343	547	GAGGAAAGAGAA AGTGATCTTTAC T[T/A]TTTTTTCAT GGAACCACCGG GGATC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4137	cg43968343	548	AGGAAAGAGAAA GTGATCTTTACT T[T/A]TTTTTCAT GGAACCACCGG GGATCT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4138	cg43968343	551	AAAGAGAAAGTG ATCTTTACTTTTT [T/C]TTCATGGAA CCACCGGGGAT CTTTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4139	cg43968343	705	AAATGGCATTAA AAATATCTACAG G[A/C]AAGGACTA CCACGAAATACA ATATT	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)

4140	cg43968343	801	CACATGTCCCATTGTATCACTATAC[A/T]TTTTTATAATAAAAAATCGTAAATT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4141	cg43987280	142	CTTGACATGCACACATATATGGATC[A/C]AAAAGTATGTACAACTAGAAAAACG	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4142	cg43987280	144	TGACATGCACACATATATGGATCAA[A/C]AAGTATGTACAACTAGAAAAACGGA	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4143	cg43987280	176	GTACAACTAGAAAAACGGACTCCAA[G/C]CAAAAATGGAAAACATGTTTCCATG	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4144	cg43274910	1083	GAGGTCACATGTAGCTGAGTGTGAA[A/gap]CCAAGAAAAATACGAAGCTTCAAAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4145	cg43274910	1125	GCTTCAAAAGTACTGTGCGTTGTAT[T/C]TCTTCATTCTCTGGCAGGCTGGGAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4146	cg43274910	393	CACTTAGAAGAATGCCTGGAACACA[T/C]TAACTTTCATTACTAATGTTTTTGG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	

4147	cg43274910	581	TCCATACACTCC CTCCACTGAGAA A[G/A]AGACAAAT GGCTTAGGCTAC AAGGT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4148	cg43918854	1838	CTGGCCAAGTCT GGCCAGCCTGG CC[C/gap]TGCAG GTCTCCCATGAA GGCCACCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4149	cg43918854	1990	GCAAGAAGGCCT CCTCAGCCCGG GG[G/gap]CTATG GCCCTGACCCCA GCTCTCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4150	cg43918854	2000	TCCTCAGCCCGG GGGCTATGGCC CT[gap/T]GACCC CAGCTCTCCACT CTGCTGTT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4151	cg43918854	2039	CACTCTGCTGTT AGAGTGGCAGCT C[C/T]GAGCTGG TTGTGGCACAGT AGCTGG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4152	cg43918854	2062	CCGAGCTGGTTG TGGCACAGTAGC T[gap/T]GGGGAG ACCTCAGCAGG GCTGCTCA	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4153	cg43918854	2067	CTGGTTGTGGCA CAGTAGCTGGG GA[gap/T]GACCT CAGCAGGGCTG CTCAGTGCC	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)

4154	cg43969669	1576	GCTGTTGCTGTT GCTGTTGCTGTT G[G/gap]GCATCT TGCTGCTAATCC TGAGGCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4155	cg43969669	1577	CTGTTGCTGTTG CTGTTGCTGTTG G[G/gap]CATCTT GCTGCTAATCCT GAGGCTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4156	cg43969669	1614	TAATCCTGAGGC TGGTAGCAGAAT G[C/gap]ACATTG GAAGCTCCCACC CCATATT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4157	cg42896238	1684	TGCTTCAGCAAA CCGGACCAGGA GG[G/gap]CCAGG GCCGGATGTGG GGACCCTCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75800 BLU PROTEIN - HOMO SAPIENS (HUMAN), 440 aa.	1.4E-227	3
4158	cg43978295	248	TATCTTACCGCA ACACCAAAGAGG A[G/gap]GCTCAG CCTTCCCCAGTT CCCTGAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4159	cg43978295	255	CCGCAACACCAA AGAGGAGGCTC AG[C/gap]CTTCC CCAGTTCCCTGA GTTCACAT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4160	cg43978295	256	CGCAACACCAAA GAGGAGGCTCA GC[C/gap]TTCCC CAGTTCCCTGAG TTCACATT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6

4161	cg43978295	342	CAGGACCAATCA ATGTCCCGGGA GG[G/gap]CAGAG AGGGTGGTGGG GCCACACTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4162	cg43978295	395	CCATATGGAAAG ACAGTATTCTCA G[A/T]TGAGGGC AGGACTTTTTTG TGGGAG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4163	cg43978295	87	CCTTTTTTTTTTT TTTTTTTTTTTT[T/ A]TAAATATTCAT TATCCTTCATTAA A	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4164	cg43978295	89	TTTTTTTTTTTTT TTTTTTTTTTTT[A /T]AATATTCATTA TCCTTCATTAAAA A	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4165	cg42913861	1886	ACCGTGTACCCC GTTCCCGCGGG GG[G/gap]CTGGA AGAAGCCCACCC GGGACTGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4166	cg42913861	448	TGCTGCTATAAA AATAACTTTTTTT [gap/T]CAAATGG CAGTTTCTGACT AATCAT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4167	cg42913861	680	GCGCTCGGCCA AGGGCAACTTCT GG[A/G]CACACG CAGATCGGCAAG TGCTATG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)

4168	cg42913861	778	GGCGGGCAGGT GAGTGGGCAGG GGC[gap/C]ACGT CCACGGCCAGC CCTGATGGCT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4169	cg42913861	802	GCACGTCCACG GCCAGCCCTGAT GG[C/T]TGGGCC CACATGGGCAAC TTCTGCA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4170	cg42913861	933	CCATCCTCAGCA GTTCAAGAATGC C[T/A]CCTCCCCG CCATTTCCTCCT GCGGT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4171	cg44932825	112	CATGCCTGGAG GTTAGTCTGGGG GG[T/C]CGGCGG GATGGACACACA GACAGAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43463 SU(VAR)3-9 HOMOLOG - HOMO SAPIENS (HUMAN), 412 aa.	9.8E-227	X
4172	cg43971224	248	ACCCCATAGACA CAGGCAGCATTA A[G/C]TCATAATT TTTAAATTAACTG TCAC	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P15907 CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,6-SIALYLTRANSFER ASE (EC 2.4.99.1) (BETA-GALACTOSIDE ALPHA-2,6-SIALYLTRANSFERASE) (ALPHA 2,6-ST) (SIALYLTRANSFERASE 1) (B-CELL ANTIGEN CD75) (ST6GALI) - Homo sapiens (Human), 406 aa.	1.5E-225	3 (3q21)
4173	cg43918561	2555	CTAGACGCAGCC CGCAGGCAGCC CC[C/A]CACCCG CCGCCTCCTGCA CCGAGAG	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3-HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224	11 (11p15.5)

4174	cg43952397	2935	TGGTCTTTCAGT CAACGTGCTAGA A[T/A]CCGATGAC TTATTAATCTCTA ATTT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4175	cg43952397	6176	CAAGAAGGCTG GGGCTGGCCCT GGG[G/gap]CTCA TCATGATGCTTT CCTGGATCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4176	cg43952397	7497	ATTCAAAGGGAC GCCAGCCATCCT T[G/A]GTGACAG GGGCCCCAACTT AGCATC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4177	cg43986954	672	AATCATTTATTTG TCTTTACAGTGA[T/C]GATGGAAGA ATGTACAGGTGT CCCC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa.	9.4E-224	18
4178	cg43984330	86	AAAGAAACGGCC TTGTCCCCAAAG G[G/gap]TCTCCT CTTGAAGGAATG GGGGCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P32121 BETA-ARRESTIN 2 - Homo sapiens (Human), 409 aa.	8.5E-223	17
4179	cg44916523	98	CCACCCTGCTTG GCCCAGGCTATG C[C/gap]TAGAAG CAAGTCAAAGGC AGGTAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	
4180	cg44916523	12	TTTTTTTTTTT[A/ T]ATTTTATTTTAC ATGAAAATCTTC C	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	
4181	cg44916523	13	TTTTTTTTTTT[A/ /T]TTTTATTTTAC ATGAAAATCTTC CA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	

4182	cg44032871	202	CAGCTTCCTGAG GAGGGGCCGGC CC[T/gap]CTCCT CTTGCCCCTGTT GAAGCTTG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4183	cg44032871	253	GCACAGGCTGG GGAGGCTGGCA CTG[C/gap]CAAC GCCATCCCTCCA TGTTGGGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4184	cg44032871	254	CACAGGCTGGG GAGGCTGGCAC TGC[C/gap]AACG CCATCCCTCCAT GTTGGGCAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4185	cg43960557	159	GCAACACTGCTT TATTAGGCCGGG C[C/gap]AGCCAG GAGCAGACACAC GGCTCCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
4186	cg43960557	174	TAGGCCGGGCC AGCCAGGAGCA GAC[A/G]CACGG CTCCTCAGTACA CATTCCCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
4187	cg43960557	2015	GTCGCGGATGG GCTGCAAGAGGT GG[G/gap]CGAAG CGCGCCTCCAC GTCCTCCAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22

4188	cg42500526	489	CGCTCTCTAGAG CCAGGCACGAC CA[C/A]TTGCTGA TTGGGGACAGG CTGTGCT	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99434 NEUROBLASTOMA - HOMO SAPIENS (HUMAN), 421 aa.	3E-220	1
4189	cg43313101	205	CTTTGCTTATTTT AAGTATTTTTTT[g ap/T]GCCTCCTGT ACAAAATACATA AAAG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q62831 NEUROGLYCAN C PRECURSOR - RATTUS NORVEGICUS (RAT), 544 aa.	1.1E-219	3
4190	cg43994920	182	CAAGTGTCCAGG CGACGTGGAAC CC[A/G]GGTGTC TTTTATGAATAAT CAAAAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15394 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-219	3
4191	cg43041368	56	ATGAGAAAAGTA CTTTATTCGTGC A[T/C]AATTTTTC AGTTCCATTCAA AATTA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15504 CG1 - HOMO SAPIENS (HUMAN), 423 aa.	1.6E-219	7
4192	cg43934903	181	TTGAGGAACCTA CGGCCTGAACCT T[gap/A]AAAAAAA AATCTCTAAAGA CCTTAC	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4193	cg43934903	190	CTACGGCCTGAA CCTTAAAAAAAA A[gap/A]TCTCTAA AGACCTTACAGT CTGCTG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4194	cg43934903	398	AAAACTATTAGA CCATATATTCTAT [A/G]TTTTTAAAG TGAATTATGCAT AAAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1

4195	cg43934903	464	ACATGATTGCAG TAACATTCTCAA G[gap/A]AAAAAA AAACCCTAGTAT ACTTTAG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4196	cg42891496	235	AAAGGCTGGCTC CCCTGGCCGAG GC[C/gap]TGGGA CTGATGCAAGAC AGCCAGCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00224 HYPOTHETICAL 46.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 409 aa.	1.3E-217	8
4197	cg43994694	985	TACCTCAGGCCC TGCGGGTGCGT CT[G/A]GAGTTCC AAGGCATTTGGG GAACCA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92554 MYELOBLAST KIAA0265 - HOMO SAPIENS (HUMAN), 401 aa (fragment).	2.1E-217	7
4198	cg43994694	1226	ACATCTGTAAGA CCACAAAAAAAA A[A/gap]TGGGTT TTACAGAATACG AAGACCA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92554 MYELOBLAST KIAA0265 - HOMO SAPIENS (HUMAN), 401 aa (fragment).	2.1E-217	7
4199	cg43261326	495	ACAGAAAAATTT AAAGTGAATGTG A[T/C]GTTGGAGA GAGTGGGAAGG AAAAGT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99984 MRNA EXPRESSED IN OSTEOBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 413 aa.	3.3E-217	1
4200	cg43917040	240	CTCATTTATACAT TCCATGCCGTCA [G/gap]GTTAAAA CTCTGCTTTGAA TCGATG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16
4201	cg43917040	241	TCATTTATACATT CCATGCCGTCAG [G/gap]TTAAAACT CTGCTTTGAATC GATGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16

4202	cg43917040	660	GCCTTCCAACCTGGCCTCCCGGAGGG[G/gap]CTTTCAGCTGGAGACCCCATTGGAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16
4203	cg43959148	375	GACATCCTTCCAGATGGTTCCCTGC[C/T]CCTAGGCCAACCTCCACAGTCATGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa.	1.4E-215	6
4204	cg43917498	199	GGCTCCAAGCACGCCATATGAAGCA[C/T]GCCAATGTCACTTATGTGCCCTGAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4205	cg43917498	446	TCACTGTGAATATCCTTTAGATTTC[G/A]TCTTGTTAACTCAGTTTTCAGTCAG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4206	cg43917498	581	CAATGTAAAGAGAGCTCGAGTGTGG[gap/G]CCAAGGCATCGGACCTTACACCTAA	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4207	cg43917498	61	TATAATCTTTATTCTATAATTCTCC[A/G]CCAGTGCTAGAATTTTCTTCCCAAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4208	cg43917498	676	TTTCTTGTCTAACAGTCTTTAAGGG[C/G]ACATAAGAAACTCACGTTAAATTTAT	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	

4209	cg43917498	703	CATAAGAAACTC ACGTTAAATTATA [T/C]CCTGACATA TTATTATTCCATG AAA	T	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4210	cg43941592	1434	CGCCCTCCTCAC CGCCCTTCCTCG G[G/C]AGTCACTT CCACTGGTGGAC CACGG	G	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07988 PULMONARY SURFACTANT-ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)) (18 KD PULMONARY-SURFACTANT PROTEIN) - Homo sapiens (Human), 381 aa.	2.1E-215	2 (2p12)
4211	cg43941592	2088	CCTGTGTAATAC AATGTCTGCACC A[A/G]TGCTAATA AAGTCCTATTCT CTTTT	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07988 PULMONARY SURFACTANT-ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)) (18 KD PULMONARY-SURFACTANT PROTEIN) - Homo sapiens (Human), 381 aa.	2.1E-215	2 (2p12)
4212	cg44006797	1111	CTGCTCTGCCCA TTTCCATTTGGG G[gap/G]CCCACA GGGCAGGGTCT GTGCTATC	gap	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE-ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4213	cg44006797	227	CGGCTTCCTCAC AAAGGAGGCAG GG[C/gap]CCCAT CACAGGGTGTCC CACCCCTG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE-ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	

4214	cg44006797	230	CTTCCTCACAAA GGAGGCAGGGC CC[C/gap]ATCAC AGGGTGTCCCAC CCCTGAAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE-ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4215	cg44006797	247	CAGGGCCCCAT CACAGGGTGTCC CA[C/gap]CCCTG AAAGGCTCTCCC AGCCTGGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE-ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4216	cg44006797	253	CCCATCACAGGG TGTCCCACCCCT G[A/G]AAGGCTC TCCCAGCCTGGA AGAGCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE-ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4217	cg44006797	296	GAAGAGCCAGAA CAAAGTGCATTG G[A/G]CCCACTC CCACCCTCTCTG AGCTGC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE-ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4218	cg43955639	1535	TTAGGACCTGAA CAGGGGTCCTG CC[A/G]GGCTGG GGACCCTCTCTG GAAACCT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.8E-215	
4219	cg43950766	390	CATTTAGTGAAC CTGCATTTCATG G[G/gap]GGGGG GGGGGGTACAC AGTATTTTA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.3E-214	22

4220	cg43950766	392	TTTAGTGAACCT GCATTTCATGGG G[G/gap]GGGGG GGGGTACACAGT ATTTTAAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.3E-214	22
4221	cg43947481	2202	ATCTTGCCATCC TCCCCTTCTGGT T[C/G]TCTGCACC CACCTGTCCCAC TGCAG	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43978 CHROMATIN-SPECIFIC TRANSCRIPTION ELONGATION FACTOR FACT 140 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 1047 aa.	8.6E-214	14
4222	cg43935715	913	GAATGTTGCCCT CCATTCTAAGGA A[T/A]GCAAAACA AATCTAAATGAT CTTCT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8
4223	cg43935715	1088	TGTCTGTAAAGC CAGGAGATTTTG T[T/C]GCCTGCTT TTGCTGCACATT AAGAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8
4224	cg43935715	823	CCTTACATCGAG TAACCCCAATTC C[G/A]CCCCCAC CCCAGTGCTCCT ACTCCG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8

4225	cg44914050	2439	GTCACACAGCTA ATGAGTTCTAAA C[G/A]GGGAACT GGACTCAGGCTT GTCTGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4226	cg44914050	55	TTTTTTTTTTTTT C]TTTTTTCCAGG CCACTTTTATTTA A	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4227	cg44914050	56	TTTTTTTTTTTTT C]TTTTTCCAGGC CACTTTTATTTAA A	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4228	cg43948829	117	CTCTCAAGAGAA AGAAGAGTTACT A[C/T]TGCAGGAA CAGACATTTTTTT AAAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4229	cg43948829	192	ACAGAAAACATT GTTATTCACATA A[T/C]AATGTGGG GCTCTGTCTCTG CCGAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4230	cg43948829	219	ATGTGGGGCTCT GTCTCTGCCGAC A[G/gap]GGGCTG GGTTCGGGCATT AGCTGTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4231	cg43948829	222	TGGGGCTCTGTC TCTGCCGACAGG G[G/gap]CTGGGT TCGGGCATTAGC TGTGCCG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2

4232	cg43948829	359	ACACGAGTCACC TCCAAAGAGCTG C[G/A]ACTGTTTG AGAATCTGCCAA GAGGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2	
4233	cg43920203	55	TTATTGGCCCAC AGAAGGGATGA GG[A/G]CGCGTG AAGGGGCTAGG GATAAGAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75065 KIAA0477 PROTEIN - HOMO SAPIENS (HUMAN), 1132 aa.	3.2E-213	1	
4234	cg43920203	57	ATTGGCCCACAG AAGGGATGAGG AC[G/A]CGTGAA GGGGCTAGGGA TAAGAATG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75065 KIAA0477 PROTEIN - HOMO SAPIENS (HUMAN), 1132 aa.	3.2E-213	1	
4235	cg43062448	124	TTAACAGTGTAA GAAGGAAAATCT C[A/C]GAAAAAGC AGATAGACAATG TAGAA	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3	(3q21.3)
4236	cg43062448	239	ACATGTGGAACT TAACTAGACCAT T[T/C]TAAGAAAG ACCAATTTCTAAT GCAA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3	(3q21.3)
4237	cg43062448	261	ATTTTAAGAAAG ACCAATTTCTAAT [G/C]CAAATTTTC TGAGGTTTTCAG ATTT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3	(3q21.3)
4238	cg43062448	262	TTTTAAGAAAGA CCAATTTCTAAT G[C/G]AAATTTTC TGAGGTTTTCAG ATTTT	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3	(3q21.3)

4239	cg43985159	1351	AAGGCATGATAGTGCAAGAGGTAAG[T/C]TTTTGATTTATAGAACATTTATAGA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15018 ORF - HOMO SAPIENS (HUMAN), 419 aa (fragment).	1.3E-212	10
4240	cg43950854	424	ATAGGCAAATTCAGAGGTGATTTCA[C/T]CATTTTCAAATTATCATCAAGAGTG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O14524 HYPOTHETICAL PROTEIN KIAA0286 (HA6800) - Homo sapiens (Human), 429 aa (fragment).	2.6E-212	
4241	cg43969195	1616	CAAGTTTGTGTATCAGAGCGGGAGT[G/T]CGGGGGAGGGAAAGAAAACAAACAG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
4242	cg43969195	289	CGGTGCGCCGGACCCACGCCGGAGG[gap/C]CGAGCTACAGGCCCTGGCGCGGGAC	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
4243	cg43999944	1878	CCGCACTCACCTGGGGGTTGGGGCA[G/A]TGCCGCGCTGTGCTGCCTGTCTTCG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4244	cg43999944	2096	GGTGGGTGCAGCCAGCGTGCGGGAA[A/C]GGGCAGGCAGCCTCCCGCTGCCAGT	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4245	cg43999944	2849	TCTGGGTCTGTGTAGCTGGGGAGAG[A/G]ATGAGGCTGCAGAGATGGGGACCAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16

4246	cg43999944	3086	CTCCCACAATTTATCCCATGAGCAA[G/T]AACCACTTTATAGCTGGCATATATT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4247	cg43984681	1347	TTGCGACACTCCCAAAGCCGTAAGG[G/gap]CCGACCCAGGCATCTTGGCCCCCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.3E-210	19 (19q13)
4248	cg43049444	168	ATCACGTAGGCCAGGAGCCTCAGCG[G/C]TGCCCCTTCAGGCTCATCTGGCAAG	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4249	cg43049444	294	GCCCTTCCCACCTGGTTGGTGACAA[A/gap]TCACAAGGTGGTAGAAGTTGCCAGG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4250	cg43049444	305	CTGGTTGGTGACAAATCACAAGGTG[G/gap]TAGAAGTTGCCAGGGACAGATAACA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4251	cg44013820	17	TTTTTTTTTTTTTTT[A/T]AAGAAGGTAGATAAATTTATTGCCA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC-LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4252	cg44013820	18	TTTTTTTTTTTTTTTA[A/T]AGAAGGTAGATAAATTTATTGCCAC	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC-LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1

4253	cg44013820	19	TTTTTTTTTTTTTTTAA[A/T]GAAGGTAGATAAATTTATTGCCACT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC-LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4254	cg44013820	955	TTAAATATATCTATTTAGTTTTTTT[T/C]TTTCCTTACCCTGAGATATTTATTA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC-LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4255	cg43934675	455	CAGTCTCTGCAGGTACCAGATTCCC[C/T]GTTGTATCCAACTGCATACATTTAC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75216 WUGSC:H_DJ1159O04.1 PROTEIN - HOMO SAPIENS (HUMAN), 379 aa.	1.1E-208	
4256	cg43932174	188	AAGCGCTGCAAAATCCCTGGCGGTG[C/gap]CCGCAATCTAACGTCTACAATAACC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4257	cg43932174	190	GCGCTGCAAAATCCCTGGCGGTGCC[C/gap]GCAATCTAACGTCTACAATAACCTC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4258	cg43932174	288	AGACGGCAAGTCGCCGCGGACGCCT[G/gap]GGGCTCTCAGCTGCTGAACAATGAC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4259	cg43932174	291	CGGCAAGTCGCCGCGGACGCCTGGG[G/gap]CTCTCAGCTGCTGAACAATGACATC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20

4260	cg43932174	82	TTTTTTTTTTTTTTT TTTTTTTTTTTTT[A /T]GCAATCTGCA AAAGACTTTATTA CA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4261	cg43995867	1354	TTGTTGTTTCTAA ATCTATATGAGA[A/T]TTGACAATAA GTATTTTTATTAT AA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4262	cg43995867	1361	TTCTAAATCTATA TGAGAATTGACA[A/gap]TAAGTATT TTTATTATAACTC AGCC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4263	cg43995867	1364	TAAATCTATATGA GAATTGACAATA[A/gap]GTATTTTT ATTATAACTCAG CCCAT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4264	cg43995867	1372	TATGAGAATTGA CAATAAGTATTTT [T/gap]ATTATAAC TCAGCCCATACA TATAT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4265	cg43995867	1379	ATTGACAATAAG TATTTTTATTATA[A/gap]CTCAGCCC ATACATATATACT ATGT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4266	cg43995867	1387	TAAGTATTTTTAT TATAACTCAGCC[C/gap]ATACATAT ATACTATGTATG CAGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)

4267	cg4395867	53	CTCGTGCCGTTA CGGCCATCACG GC[G/C]GCCGCA GTGGCGTCCTG GAGCCCTC	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4268	cg43293087	1916	GAATGGAGAAG GGTAATAGGTTG GT[gap/T]GCAGT GAATGGGCTGG GGGTGGGGT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21128 PLACENTAL PROTEIN 11 PRECURSOR (EC 3.4.21.-) (PP11) - Homo sapiens (Human), 369 aa.	2.3E-206	12
4269	cg43293087	2234	TAACCTCAATTAT GCATTTGTCCCC[C/gap]AACCCCAC TGAGAACTAAAT GCTGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P21128 PLACENTAL PROTEIN 11 PRECURSOR (EC 3.4.21.-) (PP11) - Homo sapiens (Human), 369 aa.	2.3E-206	12
4270	cg43916807	313	AGGCCAGGCTG CAGGGGCGGGC AGA[C/gap]CCTG GGCCCCGGGTC TACGCTTTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4271	cg43916807	315	GCCAGGCTGCA GGGGCGGGCAG ACC[C/gap]TGGG CCCCGGGTCTAC GCTTTCTGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4272	cg43916807	551	AAGATCTCCACT TCGGTCTGCCAT T[gap/A]AAAAAA AAAAAAATCTTTC TCTTC	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4273	cg43916807	552	AAGATCTCCACT TCGGTCTGCCAT T[A/gap]AAAAAA AAAAAATCTTTCT CTTCT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10

4274	cg43916807	565	CGGTCTGCCATTAAAAAAAAAAAAA[A/gap]TCTTTCTCTTCTTTTTCTCTTTAAAG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4275	cg43916807	565	GGTCTGCCATTAAAAAAAAAAAAA[gap/A]TCTTTCTCTTCTTTTTCTCTTTAAAG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4276	cg43916807	805	GGGGTGCAGCAGGCATGACACCAAG[G/gap]CAGAGCCCGCAGCAGGGGGCCCGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4277	cg43948416	1041	ATTGTCCATCCCATGAGGCAGGGCT[G/gap]GGCCATGCCAAGACAATCTCAAGGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4278	cg43948416	454	CCTTCCTGCCCTTGGAAATGGCGTG[C/gap]CTGGGCAATAGGGACAGGCCACAGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4279	cg43948416	455	CTTCCTGCCCTTGGAAATGGCGTGC[C/gap]TGGGCAATAGGGACAGGCCACAGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4280	cg43948416	758	CGCAGGAGGCCCCTGGAGCAGCCTG[G/gap]CCTCAGCCCAGGGCAGGTGCCCAGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11

4281	cg43920365	1326	AATGGAGAAAGA AAGCCATTTTTC C[A/G]TAAAAAGG GATGGTTCATCA TTGTG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4282	cg43920365	1468	ATCTAGACAGCC TAAATCTGATTTT [A/G]GTCTTTATA AAAATAATATCTT GTG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4283	cg43920365	2051	TCTTATGGAAAT CTCTGTTATTAA G[A/C]TATTTCAA GATGAGACAACA CTGAA	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4284	cg43920365	2188	AAGATGGGAACC TTATTTGAATGT G[T/gap]TTTTTTTT TTTCCATGATGT CCAATT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4285	cg43920365	2198	CCTTATTTGAAT GTGTTTTTTTTT [T/gap]CCATGAT GTCCAATTTTGT TGTGGG	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3

4286	cg43920365	2198	CTTATTTGAATGTGTTTTTTTTTTT[gap/T]CCATGATGTCCAATTTTGTTGTGGG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4287	cg43920365	2198	CTTATTTGAATGTGTTTTTTTTTTT[gap/T]CCATGATGTCCAATTTTGTTGTGGG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4288	cg43958860	1311	CTAATGTGATCATATGAGGACCTTT[gap/C]ATATCTGTCTTTTATTTAACAAAAA	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH) - Homo sapiens (Human), 357 aa.	6E-206	8 (8q24.1)
4289	cg44002669	333	GAGAGGCCAGGGAGGGCTGGGCGGG[C/gap]CCCCCAGGCTGGGCCGAGCAGCGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	
4290	cg44002669	338	GCCAGGGAGGGCTGGGCGGGCCCCC[C/gap]AGGCTGGGCCGAGCAGCGCAAGTAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	
4291	cg44002669	348	GCTGGGCGGGCCCCCCAGGCTGGGC[C/gap]GAGCAGCGCAAGTAGAGGAAGTCAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	

4292	cg43278557	1618	AGGCAGACCCCTCCAGAGGCCCGCC[C/gap]AGGTGGGCATGGTCCCCCATTTTCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43581 SYNAPTOTAGMIN VII - HOMO SAPIENS (HUMAN), 418 aa (fragment).	1E-204	
4293	cg43948656	39	TTTTTCTTTTTTTTTTTTTTTTTTTT[T/A]TTTAGAAGAATCAGAATTTATTTCA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB41267 HYPOTHETICAL 66.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 609 aa.	1.1E-204	X
4294	cg43302693	106	ATTCCAGCCACACCCAGGCCGTGGG[C/gap]AGCCACCTCCGAGACACCTGGGCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4295	cg43302693	137	CCCTCCGAGACACCTGGGCCGGGGG[C/gap]AGGGTCTCAGCAGAAGCGCCGTGGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4296	cg43302693	163	AGGGTCTCAGCAGAAGCGCCGTGGG[C/gap]AGCCACATCCGAGGGCACTTGGTGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4297	cg43302693	294	TCCTTTCTCAGAGAACTGGGCATAG[C/gap]CAGAGCTGGGGTGAGAAAGCCCTTC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16

4298	cg43302693	295	CCTTTCTCAGAG AACTGGGCATAG C[C/gap]AGAGCT GGGGTGAGAAA GCCCTTCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4299	cg43302693	344	CAGCCCTGCTGC ACCGAGGCTCTG C[C/gap]AGTTCT CATACCCCCTCC CCATCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4300	cg43302693	485	CTGCCCCACAGC AAGCTGCCCATG G[G/gap]CCCGGG GTCAAGCCACCA CCCACAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4301	cg43302693	535	TGTCCCAGGAGT CCGGCCAGCCC AC[C/T]ACATCCG CTCCCTAGCTCC GGCGAG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4302	cg44000884	706	TGGAAGCTGGGT TAGTTCATGCTA G[G/A]TGGCTGT AGCACTGACCTC ATGTAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43567 RING ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 381 aa.	4.8E-204	3
4303	cg44000884	939	TCAAAAGTCCTG TTTCAGTAATTTG [A/C]TTAAACTGT AGAATACTAAAA AATA	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43567 RING ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 381 aa.	4.8E-204	3

4304	cg43950996	1036	TGTAATTCCAAG AGGAGGGTGGG GA[G/gap]GCGAG GCCATAGTCTCC GAGTCCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4305	cg43950996	1044	CAAGAGGAGGG TGGGGAGGCGA GGC[C/gap]ATAG TCTCCGAGTCCC AGGACGATG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4306	cg43950996	1060	AGGCGAGGCCA TAGTCTCCGAGT CC[C/A]AGGACG ATGGCTGACAAT ACACCAA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4307	cg43950996	819	AGGTGAACGCCA GTCCAGAAAGAA G[G/gap]TGCTGG AGCCCCTGCTCT GTCCTCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4308	cg43950996	861	CTGTCCTCTCCA TCACGGTGCTCC C[C/gap]TAGGGC CTCCCCAGGCCT CCTTGGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4309	cg43950996	866	CTCTCCATCACG GTGCTCCCCTAG G[G/gap]CCTCCCC CAGGCCTCCTTG GCTCAGT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4310	cg43950996	873	TCACGGTGCTCC CCTAGGGCCTCC C[C/A]AGGCCTC CTTGGCTCAGTC CAGGTG	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1

4311	cg43950996	895	CCCCAGGCCTC CTTGGCTCAGTC CA[G/A]GTGTCTG CAGGAGGAAGG TGTTGTC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4312	cg44021565	115	GTTCATTTATTTG CTTTAAGAGTTA[C/T]ATACCATGA GACACACAGTTC TGGT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92663 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4313	cg44021565	191	CGCAGTGCTCAC GGGGAGCAAGT GG[G/A]CAGGGG ACGGTCCAGATC GATGGCC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92663 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4314	cg44021565	220	GGGACGGTCCA GATCGATGGCCA CC[C/A]ACTGAG CCGCTGCTACGT GGCCCCC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92663 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4315	cg43942842	1577	TGCATCTTCAGT TAATGTAACAGG A[T/A]AAAAAGGC AATGGATTTTATT TTAT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE,WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
4316	cg43959472	122	TTTTTTTTTTTTT TTTTTTTTTTTT[T/ G]GGCATCAGAA ATGCTGTTTATTT CT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4317	cg43959472	123	TTTTTTTTTTTTT TTTTTTTTTTTT[G /T]GCATCAGAAA TGCTGTTTATTTC TC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15

4318	cg43959472	349	CAAGCCCCCAAA TCATCAGAAAAC A[G/C]CAAGGAG CAGGAGGAGCTT GAGCAG	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4319	cg43959472	575	TTGGATTAGGAC GTCGCCCCGTTA G[C/gap]ATGCTG CCCCTGAGAGG AGAGCACA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4320	cg43968894	292	TTTTTTTTTCTT TGAATGCCAAGT[C/G]TCTTCTGTA CTTTCTTTTATTA ACA	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4321	cg43968894	428	TTAAATTTTACAT TACTCTGCCAAG[A/gap]AAAAAAAA AATTAAAACTC AAGTT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4322	cg43968894	439	TTACTCTGCCAA GAAAAAAAAAA A[gap/A]TTAAAAC TCAAGTTACTTG AAGCCT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4323	cg43968894	546	GCTCTATAAGCA GATCCAGGCCCT A[G/A]AAAGATGG GACCAGGGTATA TAATT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4324	cg43918848	1271	GGGAGCGCCCC AGAAATTCATGT CT[G/T]TGTCTGA CAACTTCAAACA GGACTT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2

4325	cg43918848	1273	GAGCGCCCCAG AAATTCATGTCT GT[G/T]TCTGACA ACTTCAAACAGG ACTTTA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4326	cg43918848	1386	ACGGGGCTGGC AGTGTCGAGAGA AC[G/A]CTCTGGA AGCTCCTAACAG ACGGCT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4327	cg43918848	1549	CTGGGGGGAGG CAGCACGGGGC GCA[gap/G]CCCT CGGCAGGCGAG CGGGCGGGAT	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4328	cg43918848	187	CTTTGGTCAAGG TGTCCCACACAT T[A/C]CCACTGCA GCTCCCAGCACA GCGGC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4329	cg43918848	231	CAGCGGCGCAC CATGAACTCGGA CG[C/T]GGAGCC CAAGGAATGGAG ATCGCAC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4330	cg43916740	1960	AAATCGCGGCCC ACAAGCATCCCC C[C/gap]ATCCCT TGCAGGCTGGG GGCTGGGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P30679 GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-15 SUBUNIT (ALPHA-16) - Homo sapiens (Human), 374 aa.	8.1E-202	19 (19p13)
4331	cg44128902	1274	AAATACCTCAGC CTCTGGTTTTTC A[C/G]CACTTGG GATTGGGGTTAA ACCTTT	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)

4332	cg43957976	975	CCTGTGTGAGTG CTGCAAGGCCAT C[G/A]ATTGTTCC TGGGAGCTTCTC CAGAC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P28906 HEMATOPOIETIC PROGENITOR CELL ANTIGEN CD34 PRECURSOR - Homo sapiens (Human), 385 aa.	7.3E-201	1 (1q32)
4333	cg43957976	976	CTGTGTGAGTGC TGCAAGGCCATC G[A/G]TTGTTCCT GGGAGCTTCTCC AGACC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P28906 HEMATOPOIETIC PROGENITOR CELL ANTIGEN CD34 PRECURSOR - Homo sapiens (Human), 385 aa.	7.3E-201	1 (1q32)
4334	cg43957976	178	ACCGTCATTGAA ACCAGGATCCCT G[C/T]TCAACCCC TCTGGAAAGAAA TCAAC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P28906 HEMATOPOIETIC PROGENITOR CELL ANTIGEN CD34 PRECURSOR - Homo sapiens (Human), 385 aa.	7.3E-201	1 (1q32)
4335	cg42914819	149	ATCCCTGTATGA ATCAAAAAGTGC C[C/A]TTCTTGCA GCTTTCTGTCAC AAGGA	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD27726 CGI-17 PROTEIN - HOMO SAPIENS (HUMAN), 385 aa.	4E-200	5
4336	cg43981683	1097	AGCCCTGGCTG GGCCTGGGGCA GGA[C/gap]CCTA AAGGGTTACTGC AAGTTCTGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4337	cg43981683	1099	CCCTGGCTGGG CCTGGGGCAGG ACC[C/gap]TAAA GGGTTACTGCAA GTTCTGGGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4338	cg43981683	213	TGGGCTTAGTGT TAAGGCGTGAAG G[G/gap]CGAGGC CAGACAGCTGGA GGCCTGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11

4339	cg43981683	219	TAGTGTTAAGGC GTGAAGGGCGA GG[C/gap]CAGAC AGCTGGAGGCC TGGTCCTCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4340	cg43981683	291	TCGGAGGCTGAA GGAAGGGCGGC GG[C/gap]ACCAC AGGGCCCTTCCC CTCTGCTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4341	cg43981683	348	CTCCTGCTCAGG CTTTCTCTCTAG G[A/C]GCATTGG AGGAATCCTCTT TCCCTG	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4342	cg43981683	390	CTTTCCCTGTCG GAAACTCAACAC T[G/A]TACAGAAC TCCAACCATAAC CCTTC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4343	cg43268635	124	TGTTCAAGCAAT TCTCGTGCCTTG G[C/gap]CTCCCA AGTAGCTGGGAC TGCAGGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA06193 SKAP-HOM - HOMO SAPIENS (HUMAN), 359 aa.	3.7E-197	
4344	cg43268635	562	ATTCTTCAGCAT CTACCAAAAAAA A[A/gap]CTCGCA TGATACACTAAA TTTAAAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA06193 SKAP-HOM - HOMO SAPIENS (HUMAN), 359 aa.	3.7E-197	

4345	cg44916575	1932	CCCAACCCTGAG AGGACAAAAACA G[A/G]AAGCCCT GTGAGTGTGGG AAAACTC	A	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16842 BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.4) (CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYL-TRANSFERASE) - HOMO SAPIENS (HUMAN), 350 aa.	3.7E-197		
4346	cg43114683	1695	TTATGATTATTTA TTAGTTTTTTTTT[g ap/T]AAATGCTTG TTCTAAGACATTT CTG	gap	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15184 PQ-RICH PROTEIN - HOMO SAPIENS (HUMAN), 400 aa.	2.6E-196	12
4347	cg44015472	115	TTTGGACCCAGG TTGCTTGGCGCT G[C/gap]CTGCCA CAGGACCCCGG GACAGACA	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
4348	cg44015472	116	TTGGACCCAGGT TGCTTGGCGCTG C[C/gap]TGCCAC AGGACCCCGGG ACAGACAC	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)

4349	cg44015472	1290	ACAGGCTCGGTCG TAGCAACAGAAG G[G/gap]CCACCG CCTCCCTGCAAC AGGGCAG				SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
4350	cg43951541	825	TTTTTTTTTTTTA AGAATAAATCAC[C/T]TTCACAAAA CTAAGACAAACT TTTT	C	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P78310 COXSACKIE AND ADENOVIRUS RECEPTOR PROTEIN - HOMO SAPIENS (HUMAN), 365 aa.	6.3E-195	
4351	cg43928808	1419	GTTCATTCATTC AACGATAGTTTC T[A/C]AACAGTAC TTAAATAGCGGT TGGAA	A	C		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q16769 GLUTAMINYL-PEPTIDE CYCLOTRANSFERASE PRECURSOR (EC 2.3.2.5) (QC) (GLUTAMINYL-TRNA CYCLOTRANSFERASE) (GLUTAMINYL CYCLASE) - Homo sapiens (Human), 361 aa.	2.7E-194	2
4352	cg43993380	2317	AACTGGTTAAAA AAGGAATAGGG GT[T/A]GAGTGTT ACAGAGAGTAGT CTGAAG	T	A		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4353	cg43993380	2463	TGCTTGCTGCTA AGAGTTTGCTAA A[C/G]TGTCATGA ATTATTCTGGTTA TTAC	C	G		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4354	cg43993380	2508	TATTACTAAAGTT TCTATGAAACAC[T/gap]TAAGTAGA TTTTAAGAATAAA TGTT	T	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	

4355	cg43993380	2509	ATTACTAAAGTTTCTATGAAACACT[T/gap]AAGTAGATTTTAAGAATAAATGTTT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4356	cg43993380	2544	TTAAGAATAAATGTTTCTGGAAAAG[A/G]ACTATGTTATGATTTTGTAGAAATG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4357	cg43967823	1470	TTAGCCCTCGCGCCCCCCGCCGTTG[G/gap]CTGCGGGAGAGCCCGCGTCCCACTC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
4358	cg43967823	1520	CCCGTGCTCGCCTCGACCCCGCGCC[G/gap]GGCACCTGTGGCTTGGGACAGATAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
4359	cg43967823	2729	TTGTATTTTTATAGACATGTTTTTT[gap/T]AAAAATCCTAAGTTTTTAAATAACT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
4360	cg43970111	889	TGCATATGCCCTCTCCACCTTAACA[T/C]CAAAATGGGGGAGGAGGAGAATTTA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43131 SYLD709613 PROTEIN HOMO SAPIENS (HUMAN), 357 aa.	6.5E-193	14

4361	cg40998719	117	CCAGGCGGGGC TGAGCTAGGGC GTA[G/C]CTGTGA TTTCAGGGGCAC CTCTGGC	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q11130 ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 7) (FUCT-VII) (SELECTIN- LIGAND SYNTHASE) - Homo sapiens (Human), 342 aa.	3.6E-192	9
4362	cg40998719	118	CAGGCGGGGCT GAGCTAGGGCG TAG[C/G]TGTGAT TTCAGGGGCACC TCTGGCG	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q11130 ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 7) (FUCT-VII) (SELECTIN- LIGAND SYNTHASE) - Homo sapiens (Human), 342 aa.	3.6E-192	9
4363	cg43985790	170	TTTTTTTTTTTTT TTTTTTATTTTT[C /T]TCTGAAGTGG TGAATTTTAATAT TG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O08746 MATRILIN-2 - MUS MUSCULUS (MOUSE), 956 aa.	4.6E-192	8
4364	cg43985790	281	TATACATATATCA AGGTAAAGTCCA [G/A]TACAAAAAA ACAGCATTTCCT ATGG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O08746 MATRILIN-2 - MUS MUSCULUS (MOUSE), 956 aa.	4.6E-192	8
4365	cg43985790	561	ACCAGGTTTCTC AGTACTGATTGT T[T/C]TACTTCAC AACATTATTGATT TAAC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O08746 MATRILIN-2 - MUS MUSCULUS (MOUSE), 956 aa.	4.6E-192	8
4366	cg43964795	364	CAAAGTTTTCAA ATGAAAACAGGT A[C/G]CCCTCTTT TCCTGTAGGCTT TCCAG	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16

4367	cg43964795	435	AGTACTTCTATTAAGGCAGCTGGAA[G/gap]CCCACCCTAGGACTTGAATGGCACC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16
4368	cg43964795	47	TTTTTTTTTTTTTTTTTTTTTTTT[T/C]TCAGGATCTTTAACTTTATTAGCAG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16
4369	cg43939832	1338	CCACCAGCCAGCAAGCATTAATGGG[G/gap]CTGGTGCCCACTTTCCACTCAGCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA06754 JM5 PROTEIN - HOMO SAPIENS (HUMAN), 360 aa.	1E-191	
4370	cg44001682	173	TCATTTTATTTTTATTAAGCACTAC[A/G]TAACACATTGCATGCTACATAATAC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O15541 ZINC FINGER PROTEIN 183 - Homo sapiens (Human), 343 aa.	3.2E-191	X
4371	cg43980381	1253	TCCCAGGGTCTGGCTGGCTGGTAGC[C/gap]AAGCACTTATGGACCAGAGTGGCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.6E-191	9
4372	cg43980381	1628	ACTGCAGTTCTCTCATGCCCACAGG[C/gap]ACTGGCCTGTGACCTTCGCAGGGGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.6E-191	9
4373	cg43920610	198	AAGAGTAGTGTGACTTTTGCTGAAA[G/gap]CAGCAGTTTTCTTCATGGAAGGAAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa.	5.9E-191	21

4374	cg43920610	334	TCATTTGCACAAGAATTTTTCAAAC[A/T]CTTTTCAAATGTGTCAACTGAGCAT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa.	5.9E-191	21
4375	cg43119894	87	CACACTGCCTGGTATACACCGCCAG[gap/G]TAGGCATTCAGAAAAGTTTCTTTTT	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA75235 LACTOSYLCERAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa.	2.3E-190	2
4376	cg43926852	1389	CATTTTCCAGAAGAGGCCCTGAGGC[C/gap]TGGAGAGGGCAAGCAGCCTACTGAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
4377	cg43926852	259	CAAGAGAGGATTTGATAAAATGAGG[A/G]AAAATGTTCTACTCTCCTTTCTTTC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
4378	cg43926852	343	AAATATACTTTCACACACATATCTG[C/T]TTCAATGGGTGCTGTCTTTCTCAAT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
4379	cg43931961	1793	GAAAAGGTAAGACCTCGTTTTAGTT[G/T]TAACTGTTTAAAAAATAACACTTGG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60256 41-KDA PHOSPHORIBOSYLPYROPHOSPHATE SYNTHETASE-ASSOCIATED PROTEIN HOMO SAPIENS (HUMAN), 369 aa.	2.9E-190	17
4380	cg43931961	2087	AACTTTGTGTTTTGGCAATCGTTTT[A/G]TAACTAAAATAAAATGAAAGCTAAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60256 41-KDA PHOSPHORIBOSYLPYROPHOSPHATE SYNTHETASE-ASSOCIATED PROTEIN HOMO SAPIENS (HUMAN), 369 aa.	2.9E-190	17

4381	cg43919278	1897	AAAATGTTTGTG TGGGAAAAAAAA A[A/gap]CTCATT GGCAGATCCAAG AATGACA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4382	cg43919278	2004	AGCAAGGCAGCT CCCCAGCCTCAC T[C/T]TTCACTCC TGATTGAGGGCC GGGTT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4383	cg43919278	2022	CCTCACTCTTCA CTCCTGATTGAG G[G/C]CCGGGTT TGTTGTCCAGCA CCAATT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4384	cg43919278	2092	AATAAACCAACA ACTTATAATTGT G[A/G]CACCAGA TGCTTAGGATCC TGGTGC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4385	cg43919278	2113	TGTGACACCAGA TGCTTAGGATCC T[G/C]GTGCTGG GTTAGCTAAGAG AATAGA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4386	cg43919278	2114	GTGACACCAGAT GCTTAGGATCCT G[G/C]TGCTGGG TTAGCTAAGAGA ATAGAC	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4387	cg43919278	2511	TTCAGGCTCCTT TTTTATAAACTG G[G/T]GATTTTTC TTTTGTCTAAAA ACAC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X

4388	cg43996402	378	CTTTTTTATTAGAAAGACAACAGTA[C/T]ATAATTTACCCCTTGCTAAAGGTAT	C	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
4389	cg43922311	226	CTGGGGGCTGGGGGCCAGGGCTCTG[G/gap]CGACCTAGAGGTGTGGACGGCACAG	G	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43293 HYPOTHETICAL 60.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 570 aa (fragment).	3.3E-189	
4390	cg43933608	2187	GAATCAACATTTAGTCTTCATTAT C[gap/T]TTTTTTTTTTTTGAGACAGAGTT	gap	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
4391	cg43933608	2201	TCTTCATTATCTTTTTTTTTTTTTT[gap/T]GAGACAGAGTTTCGATCTATTTTAA	gap	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
4392	cg44002198	218	GGAGAGGAATCGGGGTGGGGGCGCC[C/gap]GCAGCAGGGGAGAGACACTACACAG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
4393	cg44002198	323	CACACGGACACTGAAACCACGAGCA[C/T]GGCACAGCCACAGGGAGGAATGGTG	C	T		SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
4394	cg44002198	332	ACTGAAACCACGAGCACGGCACAGC[C/gap]ACAGGGAGGAATGGTGGAGCTGGGG	C	gap		SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7

4395	cg44002198	420	CTGCCACGAGTTCCTTGGCGAGGAG[C/gap]CTTGTCCGTGTTACTAAAGAGCCAC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
4396	cg44030684	1304	ACTGGTGTGCAGGTGTGAGGCTCCT[G/A]CAGGCCCACTCTCTTCAGCAGCCAC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4397	cg44030684	1422	TATCTCGAAGGGACCAGAAGTGCTG[C/T]GTGTTCAGGCCATCTCTGGCTGTCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4398	cg44030684	1755	TTCTGGGTAGGACGGTCACTGTCCT[T/C]TCTCCTGGACTGGTCTTCCCAGCCC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4399	cg44030684	2397	CCAGTGGTCCCAGCTCCCCACCCTG[G/gap]CCCTGCCCCAGCCTGTGTAGCTCTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4400	cg43935246	767	ACACTTTCATGTGGTCAATCAATTG[T/gap]TTATTGCTTTATACAGCATGATTTA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43261 HYPOTHETICAL 92.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 811 aa (fragment).	1.6E-187	14
4401	cg43935246	769	CTTTCATGTGGTCAATCAATTGTTT[gap/T]ATTGCTTTATACAGCATGATTTAAT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43261 HYPOTHETICAL 92.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 811 aa (fragment).	1.6E-187	14

4402	cg43068807	623	GATCATTATTTA GTCCTACAACCG A[T/C]GCATTGTT CCACTTTCCCAT CATTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15284 JOSEPHIN MJD1 - HOMO SAPIENS (HUMAN), 361 aa.	5.8E-187	14
4403	cg43309217	19	TTTTTTTTTTTTT TTTTT[G/T]CATG GTGAGAAGATTT TTTATTTGA	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92610 MYELOBLAST KIAA0211 - HOMO SAPIENS (HUMAN), 1267 aa.	2.4E-186	18
4404	cg43993614	133	TTTTACAAGTAG CAAAGTCCCTCC G[gap/T]TTTTTTT CCCCAGGTGAAT GTACAT	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4405	cg43993614	171	GGTGAATGTACA TGAATATAAAAA G[C/T]GGCTGAT GTCCACACTGCT CGGCCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4406	cg43993614	261	AGCTCCCGGAG CGGTGGGGCGG GGC[C/gap]TCCT CTTCTCCAGTTC CAGCACGCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4407	cg43993614	275	TGGGGCGGGGC CTCCTCTTCTCC AG[T/C]TCCAGCA CGCTCATCAGTC GTCCTC	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4408	cg43993614	281	GGGGCCTCCTCT TCTCCAGTTCCA G[C/T]ACGCTCAT CAGTCGTCCTCC TGCTG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10

4409	cg43993614	60	TTTATTTCATAGA AAGCATTTTATT[A/T]TCAGAACAG TATGGTTTTCCT ATGT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4410	cg43927276	1173	CACCTCCTTGAG AATTTTTTTTTTT[T/gap]AAGCTTAT AGTAAGGATACA TTCAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P50616 TOB PROTEIN (TRANSDUCER OF ERBB-2) - Homo sapiens (Human), 345 aa.	3.1E-186	17
4411	cg43957632	1459	GAGCGAGCGGG CGGGCGGGCAG GTG[G/gap]CACG GCCCTGCGAGC GGGAGCCGCC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
4412	cg43957632	286	TGCCGAGCTCG GTGCTGGTCTCT TT[C/A]CAAATAT AAATACGTGTGT CAGAAC	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
4413	cg43957632	300	CTGGTCTCTTTC CAAATATAAATA C[G/A]TGTGTCAG AACTGGAAAATC CTCCA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
4414	cg43922383	192	CAACGGCATCTG AAAATGGTGTGT G[G/A]CGTCGCG CGCGCCAGCTAT CGTCAG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
4415	cg43047610	185	TGGGGCCAGAA GGGTGCCTGGG AGG[C/gap]CAGG TTCTGGGGATCC CCTCCATCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB37839 TRANSDUCIN ALPHA-SUBUNIT - HOMO SAPIENS (HUMAN), 350 aa.	7.3E-185	3 (3p21)

4416	cg43950796	212	CCCGGCCCCAA GTTAGCAGCTGG GA[C/T]GATGCAA TCCTGTGAGTCG CAAGCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
4417	cg43950796	295	GCAGGCTGGAG TCCCCTGCCGCT GG[C/gap]CCTAA AATAAGCGTGCG CCATAGCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
4418	cg42269542	1339	GGGGGACAACT CCTACCGTTCTT CC[G/C]ACACAT GCCCCACTAAAC CATCTGA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14560 F25965_3 - HOMO SAPIENS (HUMAN), 903 aa.	4.4E-184	
4419	cg44001387	1331	CAGCACAATGGT GTTGCTTTAATG G[A/gap]AAAAAA AAACAGTAAAAG TGAAATA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
4420	cg44001387	1340	GGTGTTGCTTTA ATGGAAAAAAAA A[A/gap]CAGTAA AAGTGAAATATT ACTGTTT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
4421	cg43304269	235	GATGACCTCATC TTCCACTGTCCA C[A/C]GGGCACA GGGCAGACCGG GGTGCTC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75532 HYPOTHETICAL 45.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 416 aa (fragment).	8.7E-184	19
4422	cg44007066	2084	AATGCTCTCTGC AGCAGGAAATTG C[A/gap]TGAACT GAGCCTCCTTCA CTGACCT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAB50224 HYPOTHETICAL 41.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 373 aa (fragment).	1.7E-183	

4423	cg44128927	1076	GTCTGAGCTGG GACCCTGCTCCC AC[G/C]CCTGCTT CTTAAGGTCCCT GCTCGG	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.8E-183	5
4424	cg43004357	1289	TCTGGCAACAAC TCTTCCAAGGGG C[A/C]GGGGTGG GGGGGCGGGGG CGGGTAC	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4425	cg43004357	1297	CAACTCTTCCAA GGGGCAGGGGT GG[G/T]GGGGCG GGGGCGGGTAC AGGTGGAG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4426	cg43004357	1302	CTTCCAAGGGGC AGGGGTGGGGG GG[C/G]GGGGGC GGGTACAGGTG GAGAGGTG	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4427	cg43004357	1434	CTGCTGGTTCCG GGTCTCCACCCC G[C/gap]CATGGG CAGAGGCTCCG GGAGGCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4428	cg43004357	291	GCACGTGGAAGT CAAAGGGTTTCT C[T/gap]TTTTTTT TTTTTTCCCCTTT TAGAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4429	cg43004357	304	AAAGGGTTTCTC TTTTTTTTTTTT[T/gap]CCCCTTTT AGAAGCTATACA TAAAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14

4430	cg43004357	480	ATCCAACAGTTTTTTGCATTTTTTT[gap/T]AAATTAATTTTTCATTTTTTTAAAA	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4431	cg43004357	87	ATAGTCGTTACAAAAAGTTTTTTTT[T/gap]CTTTTAAATAAATTCACACAAAGAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4432	cg43004357	850	ATGGCGTGAGTGCTCTAAGGATAGA[C/gap]CTACGGTATTCTAGAGCAAAAACCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4433	cg43004357	966	GCTCACCCCTTACTTTTTTTTTTTT[T/gap]AGCTTTTCTCTCATTTTTTTTTTGT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF-RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4434	cg43919094	365	CCTAATAATAGAGATCTGAGGTGGT[C/T]ACCAGGAGACTACGTTCTTTTGATT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76004 ATP(GTP)-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 358 aa (fragment).	9.9E-183	2
4435	cg43919094	454	AAAACTTGAAGTTGTAGGCTTGGAA[G/C]AGTATCAGCTCAGTATATCCTTCCT	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76004 ATP(GTP)-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 358 aa (fragment).	9.9E-183	2
4436	cg43959681	2439	ATACAGAGAAGGGTCTTTTTTTTTT[T/gap]AAGTATTTCAGTGAAAACTTGGTGT	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43684 SPLEEN MITOTIC CHECKPOINT BUB3 - HOMO SAPIENS (HUMAN), 328 aa.	6.8E-182	10

4437	cg43959681	262	GGAAGCAAGGAGGCGGCGGCGGCCG[C/gap]AGCGAGTGGCGAGTAGTGGAAACGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43684 SPLEEN MITOTIC CHECKPOINT BUB3 - HOMO SAPIENS (HUMAN), 328 aa.	6.8E-182	10
4438	cg43959681	2565	TATGGAAAGCTTTGTTTGCTTCCTA[C/gap]AAATACATGCTTATTCCTTAAGGGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43684 SPLEEN MITOTIC CHECKPOINT BUB3 - HOMO SAPIENS (HUMAN), 328 aa.	6.8E-182	10
4439	cg43986952	182	ATCGTCGTTTTCAATATTACAAAAA[A/gap]AGGAAGAAAAATACAAGGGAAGCAG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR-INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa.	2.9E-181	19 (19q13.1)
4440	cg43986952	183	TCGTCGTTTTCAATATTACAAAAAA[A/gap]GGAAGAAAATACAAGGGAAGCAGA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR-INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa.	2.9E-181	19 (19q13.1)
4441	cg43945307	241	CGGGGTGGGGGAGGGTGTGTCAGTC[T/gap]GCAGAGAAGCTCCTGGGAGAATGGA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa.	3.7E-181	3
4442	cg43923337	1106	AGACAAAACATGACTGAAAAGAGCA[C/T]CTGTACTTTTCAAGCCACTGGAGGG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14
4443	cg43923337	1133	TGTACTTTTCAAGCCACTGGAGGGA[G/A]AAATGGAAAACATGAAAACAGCAAT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14

4444	cg43923337	1196	CTGAATAATCAAAGACTAATTTGTG[A/G]TTTTACTTTTTAATAGATATGACTT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14
4445	cg43923337	1253	CAACATGGAATGAAATAAAAAATAA[A/G]TAATAAAAGATTGCCATGAATCTTG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14
4446	cg43989631	293	ACAGGGGAGAGAAGGGGCAGGGAAG[G/T]CCTGGGGGAGGGAATGGCAGACCCC	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75056 KIAA0468 PROTEIN - HOMO SAPIENS (HUMAN), 384 aa.	1.6E-180	
4447	cg42717910	327	CACGCCGCTCCCCATCCCCGCAGCG[C/gap]GTCTGCACCGGAGACTCTGCGGGGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60547 GDP-MANNOSE 4,6 DEHYDRATASE - HOMO SAPIENS (HUMAN), 372 aa.	2.1E-180	
4448	cg43950166	2824	AATTTTAAAGCATCATATAAATTAA[A/C]GGTGTCATTGGTAATAATCTCATAT	A	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92623 MYELOBLAST KIAA0227 - HOMO SAPIENS (HUMAN), 336 aa (fragment).	1.9E-179	14
4449	cg43928466	1637	AAAAATATAATAATCATAAAGTCTG[A/T]AACAGGACATCGCCTTTGGGAACTA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76091 NITRILASE HOMOLOG 1 - HOMO SAPIENS (HUMAN), 327 aa.	2.4E-179	1
4450	cg43928466	1639	AAATATAATAATCATAAAGTCTGAA[A/T]CAGGACATCGCCTTTGGGAACTAGA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76091 NITRILASE HOMOLOG 1 - HOMO SAPIENS (HUMAN), 327 aa.	2.4E-179	1

4451	cg43267504	1425	GCCATAAAATGTGCTTCTCTTCTTC[A/G]GGATGTTGTTTGCTGTCTGATCTTT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q01638 ST2 PROTEIN PRECURSOR - Homo sapiens (Human), 328 aa.	4.9E-179	11 (11p14.3)
4452	cg43944312	427	TCTACCTTGAGGCGTGCTGGCTGGG[C/gap]CCCGTTTCCACACCAGCACATGGTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	4.4E-178	17
4453	cg30490224	1906	TAGATTCGGTTACAATAAAACAGCA[A/G]ATGCACCAGAGACACAAGGCTTGAA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4454	cg30490224	1907	AGATTCGGTTACAATAAAACAGCAA[A/G]TGCACCAGAGACACAAGGCTTGAAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4455	cg30490224	3110	CAGAGCCTCAATTATTAAGGAAAAG[gap/C]TCTTCAGGAAAAATACTAAAATATT	gap	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4456	cg30490224	3137	CTTCAGGAAAAATACTAAAATATTT[T/gap]CTCTTCCTCATAAGCTTCTAAATTA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4457	cg30490224	3327	ACACAGGTCTAAACTCAGCATGCTT[T/gap]GGTGAGTTTTTCTCCAAAAGGGGCA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)

4458	cg30490224	3346	ATGCTTTGGTGA GTTTTTCTCCAA A[A/gap]GGGGCA TATTAGCAATTA GAGTTGT	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4459	cg43984598	296	ATCCCAGGTACT GCTTTTACTACT G[T/G]GATTTGTT GCCAGCATTTAT AACTT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC33734 CELL DIVISION PROTEIN - HOMO SAPIENS (HUMAN), 327 aa.	1.5E-177	X
4460	cg43969747	1870	GCACGGGCCCT AGAGCTGAACG GCA[G/gap]GGGT CAAAGGTCAGAG CATCTGCAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4461	cg43969747	1873	CGGGCCCTAGA GCTGAACGGCA GGG[G/gap]TCAA AGGTCAGAGCAT CTGCAGAGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4462	cg43969747	313	GCGGCTGATTTA TCTCTGCATCTT C[A/T]TTTTTTTC CCGAGCAACATC TGCGT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4463	cg43969747	318	TGATTTATCTCT GCATCTTCATTTT [T/C]TTCCCGAGC AACATCTGCGTG TCGG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4464	cg43969747	333	TCTTCATTTTTTT CCCGAGCAACAT [C/T]TGCGTGTCG GTCTGCTTTTATT ACC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16

4465	cg43969747	382	CCTCCCAGACTG AGCCCCCGACCT G[G/gap]CCCAGC CTGGCCCGTCC CCAATCCA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4466	cg43969747	415	TGGCCCGTCCC CAATCCAGTGGG CT[G/gap]GCCAG GCCACCTGCACC AGGGAGGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4467	cg43969747	541	ACGCGGGCAGG GAGGGGCAGAG AAC[G/A]CACTAG CTTGGGGGTGG GCACCAGC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4468	cg43969747	566	GCACTAGCTTGG GGGTGGGCACC AG[C/gap]CTCAG ACCCCTCAGCAG CTTTGGGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4469	cg43972734	437	TTTTTTTTTCCTG CTTTCTGCTTA[A/G]AACAAATAT GGGCTTTCTTTT TGCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15555 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 327 aa.	8.3E-177	18
4470	cg44035397	446	ACTGGAATCTTT CTTCTCAACAGG G[G/gap]CTGCAG GGTCTACCCCTC CGACTCT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa.	1.7E-176	7
4471	cg43933591	1024	GGCTAGGGACC CAGGGCAGAATC TA[C/T]ACGGTCC AAGGGGAGGGA CGGTGTT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8

4472	cg43933591	1763	TCACGCCATAAGTGGAATTCTTCAT[C/T]GAGTCGTTGACTTCTCGACGGAATG	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8
4473	cg43933591	728	CCACACGCATACATCCACACACACT[G/gap]CCTCGAGGGCTGGGGAAGACTAAAA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8
4474	cg43938932	400	GAGGCCTAGTTAAGAATTCCTTGCC[C/T]TAGTGGTGAACAAGGACTAAACACA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA24081 EXTR2 PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.2E-176	1
4475	cg43985951	132	TAATATTAGTAATTAAATAGCAACG[C/T]TCATCCCCCAACCGGAATGTACAAC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q99501 GAR22 PROTEIN - Homo sapiens (Human), 329 aa.	2.2E-176	22 (22q12)
4476	cg43985951	87	GGTCTTCAGAACACCGGGCTCGCCC[gap/G]CCTCCTCTAAGGCATTCAATAATAT	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q99501 GAR22 PROTEIN - Homo sapiens (Human), 329 aa.	2.2E-176	22 (22q12)
4477	cg43985951	87	GGTCTTCAGAACACCGGGCTCGCCC[gap/G]CCTCCTCTAAGGCATTCAATAATAT	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q99501 GAR22 PROTEIN - Homo sapiens (Human), 329 aa.	2.2E-176	22 (22q12)
4478	cg43313822	407	TTTCATGATGTTGCATAGGCTGGCA[T/C]GGAATTCCAGGGCTCAAGTGATCCT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P16260 GRAVE'S DISEASE CARRIER PROTEIN (GDC) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG) - Homo sapiens (Human), 332 aa.	9.5E-176	10

4479	cg43989723	1552	ACTGTGCCTTGT TGTCTGCTGGGG G[G/gap]CCATAG CTGGCACTGCCC ACCGTAA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
4480	cg43989723	1562	GTTGTCTGCTGG GGGGCCATAGC TG[G/gap]CACTG CCCACCGTAAAG GCCCTCGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
4481	cg43967060	151	TGGGACAAGGG CATGAGGGGCG TGG[C/gap]CCCC CAGCAGGCAGC GGCGGTTCCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P04899 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), 354 aa.	4.1E-175	3 (3p21)
4482	cg43967060	859	AGGCTTCAAACA GGGAGGCCTGT GG[C/gap]AACCC CTCCCCTACGTC TGGAGCTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P04899 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), 354 aa.	4.1E-175	3 (3p21)
4483	cg43919107	101	AGATGAGGTCCC CTTCTCGGTGGA A[C/gap]CCCCAC ACCAGTGCTCTT CCCATGC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q11206 CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFER ASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4) - Homo sapiens (Human), 333 aa.	1.1E-174	11
4484	cg43967532	2654	CCTGGTCCCTTT GCTGTCACTATT A[C/G]ATAATGGA CTTGCACTTTTC CTCCC	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8

4485	cg43967532	3127	GATTACAATGTC CACTACTGACAG G[C/gap]GCAGTG CGTGTGTGTGAC CCACCGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4486	cg43967532	3147	ACAGGCGCAGT GCGTGTGTGTGA CC[C/gap]ACCGG GTTCCCGGGCA CTGTCCCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4487	cg43967532	3150	GGCGCAGTGCG TGTGTGTGACCC AC[C/gap]GGGTT CCCGGGCACTG TCCCCCCCG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4488	cg43967532	688	CCCAGGACTCTA TCCAGAATGATT A[T/C]TGTAAAGC TTTACAAATCCC ACCTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4489	cg43967532	90	AAAAGCATGAAA ATAAAATGAACA C[G/A]TACGGGA ATTACTATTAACA TAAGC	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4490	cg43980846	294	AATCCGGCACAA GCTCTGTCTGTG C[G/C]ATCAAGG CTGACCCAGCAG CCTCAA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P35212 GAP JUNCTION ALPHA-4 PROTEIN (CONNEXIN 37) (CX37) - Homo sapiens (Human), 332 aa.	2.8E-174	1 (1p35.1)
4491	cg43919276	1331	GAGGCAATAAAG ATATTTGGCCTT C[A/T]AAAAAAAA AAAAAAAAAAAA AAAAA	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD48057 RING FINGER PROTEIN AO7 - MUS MUSCULUS (MOUSE), 456 aa.	3.7E-174	

4492	cg43083550	3035	CTGGGGTGGTG GCTCACGCCTGT AA[T/C]CCCAACA CTTTGGGAGGCC AAGGCA	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15430 LEUKOCYTE ANTIGEN CD84 - HOMO SAPIENS (HUMAN), 328 aa.	9.8E-174	
4493	cg43250735	298	AAGGGTGAACAC TGATTTTTTTTTT[T/gap]CTTTTTAG AAACAAAAACCA TCCAC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B426B) - Rattus norvegicus (Rat), 485 aa.	1.2E-173	9
4494	cg43250735	384	ATCATCGCATAA ACTGAACATACG A[A/gap]GTTACC ACCTCAAGGGAA TAACAGA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B426B) - Rattus norvegicus (Rat), 485 aa.	1.2E-173	9
4495	cg43918085	242	GGGGGCAGGAG CAACTTGTAATA AT[T/G]AAAATGT AAACGTGAAAAA AAGGAT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.9E-173	
4496	cg43918085	263	AATTAAAATGTAA ACGTGAAAAAAA[gap/A]GGATGGA ATAAAAGTCCCT ACTTAT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.9E-173	
4497	cg43281313	1153	TTCAATTTTCTTT CTGAGCCAGACT [A/G]GTTTACGCT ATTCAAATCTTTT CCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99496 DING GENE - HOMO SAPIENS (HUMAN), 336 aa.	2.5E-173	1
4498	cg43281313	1430	TTAAATATTATGT ATTCTGACTTTT[gap/A]TTTTCCCC CGGAGTCTTGTA TATTT	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99496 DING GENE - HOMO SAPIENS (HUMAN), 336 aa.	2.5E-173	1

4499	cg43281313	1632	ATTGTCATGCAA TGTTTTTTTTTTT[gap/T]CCATTCTT TTTCCCTGTAATT TTGG	gap	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99496 DING GENE - HOMO SAPIENS (HUMAN), 336 aa.	2.5E-173	1
4500	cg43928859	1097	CCACAATAGGAA CATCAAAAGAAA A[T/G]TTCAAGT TTGATTTTTTTTT CTTT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4501	cg43928859	1145	TTTTTTCCTTTCT TAAAAAAAAAA[A/gap]GGAAGTAA ATAAATTAAATTG CCAA	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4502	cg43928859	1226	TTCTTAAAAAAAA GAGGGGGGGGG G[gap/G]CAGTAG GTGGAGTTTGTG AAATATA	gap	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4503	cg43928859	1355	TGGCCTGTGCCA CAAGAGGCAGT GC[C/gap]AACCA TATTTTAGCAAAA GCTAGGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4504	cg43930118	101	CTCTGTAATACA ATGTGGTGAAAA C[G/A]TCTTAATT CAGGACATCTTC CACCT	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD17940 SUCCINYL-COA SYNTHETASE ALPHA SUBUNIT (EC 6.2.1.5) - HOMO SAPIENS (HUMAN), 331 aa.	1.8E-172	2
4505	cg44000768	1448	GCGCCTCAGCC CTGGACTGTTAG AG[G/A]TGCTGC AGCTGCTCCTGC TCTCTGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75500 PUTATIVE GLIALBLASTOMA CELL DIFFERENTIATION-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	9.1E-171	9

4506	cg44000768	1458	CCTGGACTGTTA GAGGTGCTGCA GC[T/G]GCTCCT GCTCTCTGATCT TATTGCT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75500 PUTATIVE GLIALBLASTOMA CELL DIFFERENTIATION-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	9.1E-171	9
4507	cg43923012	101	CACTCCAACATA AAAAGTAGAATT C[A/G]CCCACTTC CACTTAATATTCT ATAG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.1E-171	X
4508	cg43923012	149	TAGAATGAAGTT GTACCACAAACC A[T/C]AGTAACTT ACACAGGGGGA AAAGTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.1E-171	X
4509	cg43923012	161	GTACCACAAACC ATAGTAACTTAC A[C/gap]AGGGGG AAAAGTTACTGA AATAAAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.1E-171	X
4510	cg43925222	4156	TAGGAAACCCTT TGTGTATCTTTTC [T/A]GACTGGGAT GGGGGCTGAGC ATGCT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4511	cg43925222	4164	CCTTTGTGTATC TTTTCTGACTGG G[A/G]TGGGGGC TGAGCATGCTTG TGCAGA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4512	cg43925222	4449	TTAGTGCTCAAT AATATAAGACCT G[T/G]TGTTATTA GAACGAGTCTTT CTTAT	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7

4513	cg43925222	4506	ACAGAGCAGGTA TATGCCTGTTAG A[T/C]CTTAGCTG TGGGGTTCCTTT ACTAT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4514	cg43925222	4757	TCTTCAGTTGAG CTCTCAGCCTTA G[T/G]AAGGAAG CACGTGGAGGA GGGACGG	T	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4515	cg43941339	1563	CGAGTCTGGTCC CGACGATGCTGT G[C/gap]TCTGCC TCCTCCTGCTGC TGCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa.	8.2E-170	4 (4q21)
4516	cg43251632	300	CTCCCACCACGC CGGGCAGGCAC AG[C/gap]CATCT TTTTAAAATCCG CGCTGATT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.5E-169	
4517	cg43251632	301	TCCCACCACGCC GGGCAGGCACA GC[C/gap]ATCTT TTTAAAATCCGC GCTGATTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.5E-169	
4518	cg44032718	152	ACGCACCCGGG AATCGCAGGAG GAC[A/G]AGGCT CAGCTCTTGCCA GGCCAAAT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.7E-169	X

4519	cg43926685	999	GGAAAGCTAAGAGGAAGATTCAATA[gap/A]TTAACTAGCTTGAAGCCTGACCTAG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4520	cg43926685	999	GGAAAGCTAAGAGGAAGATTCAATA[gap/A]TTAACTAGCTTGAAGCCTGACCTAG	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4521	cg43926685	1032	GCTTGAAGCCTGACCTAGCCAGAAG[A/gap]AGTGCCTGTCCGCTGCAGCCGCACC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4522	cg43926685	1033	CTTGAAGCCTGACCTAGCCAGAAGA[A/gap]GTGCCTGTCCGCTGCAGCCGCACCC	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4523	cg43926685	1104	GTGTGTCTGGAACACGCTGCTCCCC[C/gap]TGGGGCAGCTGTTGGGATTCTGATT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4524	cg43926685	1109	TCTGGAACACGCTGCTCCCCCTGGG[G/gap]CAGCTGTTGGGATTCTGATTAAAAG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)

4525	cg43926685	1133	GGCAGCTGTTG GGATTCTGATTA AA[A/gap]GAGGG GAAACGATCATC CTGGACAG	A	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4526	cg43987324	279	TGGCCCCCCAAA ACCTAACCTATC T[G/C]ACAATCAA TAATCATCTTTTG ACTA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD41895 ASB-3 PROTEIN - HOMO SAPIENS (HUMAN), 518 aa.	3.8E-168	2
4527	cg43959938	456	CCCTCTAGAGTT C[T/C]GTAGGATG AATTTCAGCACT GCAGG	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.2E-168	X
4528	cg43280431	1032	TTCGGAATTTAG AACCCATCTATG A[G/T]AGAAAGTT CAGTCACTTTAT TTATT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA83025 KIAA1073 PROTEIN - HOMO SAPIENS (HUMAN), 643 aa.	2.9E-167	
4529	cg43942787	1269	ACTGGCATTTTG AAGGCATGGCC CA[A/G]GAGAAG AGACACTAGCCA TAAAATC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15327 NUCLEAR PROTEIN - HOMO SAPIENS (HUMAN), 319 aa.	3.6E-167	10
4530	cg43329903	1372	ACACCTCATTCT GGCCGAGAGTA GG[G/gap]CAGCT GCCTCCAGACTC TGGGGAGA	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.9E-167	12
4531	cg43949591	699	CTCTTTCACATC TGGGCACACGTC T[G/gap]CCTTCA GGCTGTAAGAAT TTCATTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.6E-166	18

4532	cg43949591	798	TCTCATCCCTTC CATAAGGAAAAT G[C/gap]TCTGCC AATTCAAGTTTC ATTCAGT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.6E-166	18
4533	cg43996522	156	AGAACATAATTC TTTCCCAGAAGG G[G/gap]AAGGGG GAGCTATACTTA ATCGGAT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P56180 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - *Homo sapiens (Human)*, 551 aa.	3.3E-166	
4534	cg43924431	1490	GCTCATCGCCAT AGCAAACCCGC GG[G/A]TGCGCA GCGTGGGGCCC CG	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4535	cg43924431	253	ATAAACTACAAC ACCCTTCTCACA G[C/G]TCATAAAA TTACCAATAATTA TCCA	C	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4536	cg43924431	353	ACCGTGCTGGC CTCCCACCCCCA CC[C/T]CAGTCTT TTACAGATGGTT TTTCAA	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4537	cg43924431	596	GCTCTATGCCAG CATTTCTCCTTAA [T/A]TTAAGGAAT GTGAGCACCTTC CTTC	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4538	cg43926509	8012	TCTACAGGACGA ATTGAGGCTTAA A[C/A]TTTACTGT TAATGATACTGG TTCAT	C	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15165 CLONE 22 - HOMO SAPIENS (HUMAN), 306 aa.	4.2E-166	18

4539	cg43962058	308	AGTACAATCCAG TATATGCAGAAA G[G/C]TACTCAG CATCACACTCGT GATCAA	G	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75880 H-SCO1 - HOMO SAPIENS (HUMAN), 301 aa.	4.8E-165	17
4540	cg43962058	736	CGCAGGCAGGA ATGCACTGGCTG TG[C/gap]CTCGC CCCGCCATGTCC TTCCACAG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75880 H-SCO1 - HOMO SAPIENS (HUMAN), 301 aa.	4.8E-165	17
4541	cg43951985	385	AAGAGACAAATG GAAACATTCCAT T[T/A]CCTTATTG AACAGAACTTTC TTCAT	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4542	cg43951985	588	TCCCTTTCCAAA GGTGGGCAATGT G[C/gap]CTCTTC CTGGAAGGTTAT TTTACAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4543	cg43951985	601	GTGGGCAATGTG CCTCTTCCTGGA A[G/gap]GTTATTT TACAAGCACGGG CCCCTG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4544	cg43951985	709	GCAACTTGTCCC GCCTTGAGTCTG A[T/C]GTCAGAAG AGCATGTCAGTC CACTT	T	C			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4545	cg43936047	1255	CTGTGCACAAAC GTTTTATACTAAA [T/A]AAATATCAA ACTACATTCTTCT GAA	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13

4546	cg43936047	1574	GACTCAAAATTTTGGAGTGGTTGGC[G/A]TGCCTCTCTTCATTTTACTTTTTGA	G	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13
4547	cg43936047	1578	CAAAATTTTGGAGTGGTTGGCGTGC[C/gap]TCTCTTCATTTTACTTTTGACTGG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13
4548	cg43936047	669	GAGAAGAGGCCCAAGTGGCTAGCCA[A/G]TTCATTGCAGATGTCATTGAAAATT	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13
4549	cg44003630	1615	GCTGCCGACAGCCAAGACGTACTGG[G/T]AGGAGAAAGCGCCGCCGTGAGCCTG	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4550	cg44003630	1621	GACAGCCAAGACGTACTGGGAGGAG[A/G]AAGCGCCGCCGTGAGCCTGGGTCTC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4551	cg44003630	1622	ACAGCCAAGACGTACTGGGAGGAGA[A/G]AGCGCCGCCGTGAGCCTGGGTCTCC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4552	cg44003630	183	GCAGGAAGATCCAACCCCTCAAAGC[A/T]GGTGGCATGGGTGCCACTGGGAGGG	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	

4553	cg44003630	190	GATCCAACCCCT CAAAGCAGGTG GC[A/G]TGGGTG CCACTGGGAGG GGATCTGG	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4554	cg43945743	1071	TGAGTCCCAGCA TTCACTTCTCAC A[C/T]GGGCTTCT CCAACGTGGCA GCGGCC	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4555	cg43945743	1333	TCCTAGTTTAAA AAAAAAAAAAAA A[gap/A]GTCTTCT TAACCCTGATGC TGTCTC	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4556	cg43945743	1354	AAAAAGTCTTCT TAACCCTGATGC T[G/gap]TCTCCC GACCATAGATTA GGGAAGC	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4557	cg43945743	1519	TTAGACCTCCCC ACGAAACAAAGT G[G/gap]ACTCCT GTCCCCTGCCAC TCAGCGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4558	cg43945743	1531	ACGAAACAAAGT GGACTCCTGTCC C[C/gap]TGCCAC TCAGCGGCCAC CCCCCCAA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4559	cg43945743	1615	TGTGAGCCCCAA GCCCCACCCGC AG[G/gap]ATCTT CCAGCCACATGA GGCCATTT	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)

4560	cg43945743	18	CGTTTTTTTTTTTTTT[G/T]CCCGAAATGACAAGTACCGTTTATT	G	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4561	cg43945743	314	AAGTGCAGGAGCCCTGGGCTGGGGG[G/gap]CCTCTGGCCTCTGCAGCCGGGTGGG	G	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4562	cg43945743	73	TTACACAAATGAACCCAGCCTCTGG[C/gap]TTGGGCACCGTCCCACGGACCAGCA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4563	cg43945743	859	TCCAGCCCAGGGCCCAGGGTGGGGC[C/gap]ACAGGAGCTAACGGAGAACCTGGCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4564	cg43920818	1929	AGAAGTAAAAACTCAGAATGTAAAA[A/T]CTTGTTTCCTTTCAGTTTATTAAAT	A	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15390 HYPOTHETICAL PROTEIN KIAA0009 - Homo sapiens (Human), 314 aa.	3.9E-163	8
4565	cg43963378	158	GAAAAATTAGGACTGGAGGGGGCAC[C/gap]AGTTCTTCCTAAGGGGAGCTTGAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75064 KIAA0476 PROTEIN - HOMO SAPIENS (HUMAN), 1386 aa.	7.4E-163	1
4566	cg43922270	1062	TGAACAAGGGTGCCCATGTGGTTGC[C/T]CCTTCTGTCATCCAGAGAAAGTGCT	C	T			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2

4567	cg43922270	777	AGTAGAGTCTTTTTTTTTTTTTTT[T/gap]TACATTTGTCATTTAAGAAGGCTGC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2
4568	cg43922270	778	GTAGAGTCTTTTTTTTTTTTTTTT[T/gap]ACATTTGTCATTTAAGAAGGCTGCC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2
4569	cg43922270	802	TTACATTTGTCATTTAAGAAGGCTG[C/gap]CCTGCGGTATTCATAATTCATTGTT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2
4570	cg43949225	184	GATTGTTTGCCTTGGATGCCCCTGG[C/gap]AAATCTCGTGAGGCATTGAACTAGA	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P05198 EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2- ALPHA) - Homo sapiens (Human), 314 aa.	1.3E-162	14
4571	cg43997225	1871	AACTGCAAAGGGATGCTGTATAGCA[A/G]CACATCAGAAGTCGGAAGGAACTGA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15777 FETAL BRAIN PROTEIN 239 (239FB) - Homo sapiens (Human), 294 aa.	2.1E-162	11
4572	cg43997225	2048	TAAATACCCCAAGTTGTCTTCTTAC[T/gap]TCCTCTCCCCTCTCCCATTTTGCAC	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15777 FETAL BRAIN PROTEIN 239 (239FB) - Homo sapiens (Human), 294 aa.	2.1E-162	11
4573	cg43248117	1226	GAGTAAATGAGGGAGTCCAGTCCCC[A/G]GTGAACTCTCCTTTTGTGCTTATCA	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14894 MU-CRYSTALLIN HOMOLOG (NADP-REGULATED THYROID-HORMONE BINDING PROTEIN) - Homo sapiens (Human), 314 aa.	1.2E-161	16 (16p13.11)

4574	cg43965825	1557	AGGCATATTTGAGCTCCACATTAAC[C/gap]TTGCGGCAGGCGTCTACTTGCTCTG	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P17936 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3) - Homo sapiens (Human), 291 aa.	1.9E-161	7
4575	cg43965825	376	CTCAGTCATGGCCACAGTTGTATCA[T/A]ATAGCATCTCTAACATTTCATCTAG	T	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P17936 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3) - Homo sapiens (Human), 291 aa.	1.9E-161	7
4576	cg43957287	162	GGGGCAGGGGTTTCAGGGGGCTCAG[C/gap]CTCTTCATGGGGCAGGCCTCAGCCC	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB46375 HYPOTHETICAL 40.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 352 aa.	2.4E-161	3
4577	cg42712022	1386	TTAGAGGAAACACATAGAGCTGGAA[C/gap]CTGTTAATGGAAAGCAGTCACAGCT	C	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.4E-161	9
4578	cg42712022	1415	TTAATGGAAAGCAGTCACAGCTGAG[T/gap]TTTTCGGAGAACCAAGGAAATTAAA	T	gap			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.4E-161	9
4579	cg43993462	344	ATAGAGCTCACGGATACAGAGGGCC[A/G]ACTGTCTATGACGTTAAACATCTAC	A	G			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
4580	cg43993462	615	TGGAACTGTAGTCTCACTTCTTACC[gap/A]AAAAAAAAACAATGAACTGGATTCA	gap	A			SILENT-NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5